

361 TTCCGCCAGATTGTGTCTGGCTGGACTTCTGCCACAGACTACTCCATCTGCCACAGAGAC 420
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361 TTCCGCCAGATTGTGTCTGGCTGGACTTCTGCCACAGACTACTCCATCTGCCACAGAGAC 420
Qy
421 CTAAGCCCGAGAACCTCTCTTTTGGATGAGAAAAACAACATCGCATTTGCAGACTTCGGC 480
Db
421 CTAAGCCCGAGAACCTCTCTTTTGGATGAGAAAAACAACATCGCATTTGCAGACTTCGGC 480
Qy
481 ATGGCGTCCCTGAGGTGGGGGACAGCTCTCTGGAGACAGAGTGGGGTCCCGCCATTAT 540
Db
481 ATGGCGTCCCTGAGGTGGGGGACAGCTCTCTGGAGACAGAGTGGGGTCCCGCCATTAT 540
Qy
541 GCCTGTCCAGAGGTGATTAAAGGGGGAATAATGATGGCGCGCGGACAGACATGTGGAGC 600
Db
541 GCCTGTCCAGAGGTGATTAAAGGGGGAATAATGATGGCGCGCGGACAGACATGTGGAGC 600
Qy
601 TGTGGAGTCACTCTCTCGCGCTCTCTGTGGGGGCTCTGCCCTTTGATGACGACAACTTC 660
Db
601 TGTGGAGTCACTCTCTCGCGCTCTCTGTGGGGGCTCTGCCCTTTGATGACGACAACTTC 660
Qy
661 CGCCAGCTGTGAGAAAGGTGAACCGGGGGCTCTTCCACATGCCCACTTCATTTCTCCA 720
Db
661 CGCCAGCTGTGAGAAAGGTGAACCGGGGGCTCTTCCACATGCCCACTTCATTTCTCCA 720
Qy
721 GATTGCCAGAGCTCTCTGAGGGGAATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTG 780
Db
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Qy
781 GAGCAAAATTCAGAAACATCTTGTGTACTAGGGGGGAAAAACAGAGCCAGACCCGTGGCTG 840
Db
781 GAGCAAAATTCAGAAACATCTTGTGTACTAGGGGGGAAAAACAGAGCCAGACCCGTGGCTG 840
Qy
841 GAGCAGCCCTGCGCGCGGTAGCCATCGGAGCGCTGCCATCCCAACGAGAGCTGGAC 900
Db
841 GAGCAGCCCTGCGCGCGGTAGCCATCGGAGCGCTGCCATCCCAACGAGAGCTGGAC 900
Qy
901 CCCGAGCTCTAGAGAGCATGGCATCTGGGCTGCTTCAGGGACCGCGAGAGCTGCAT 960
Db
901 CCCGAGCTCTAGAGAGCATGGCATCTGGGCTGCTTCAGGGACCGCGAGAGCTGCAT 960
Qy
961 CGCGAGCTGCGCAGTAGGAGGAGAAACAAGAAAGATGATATATATCTGCTTTGGAT 1020
Db
961 CGCGAGCTGCGCAGTAGGAGGAGAAACAAGAAAGATGATATATATCTGCTTTGGAT 1020
Qy
1021 CGGAGGAGCGGATCCAGCTGTGAGGACAGACCTGCTCCCGCGAATGATGTTGAC 1080
Db
1021 CGGAGGAGCGGATCCAGCTGTGAGGACAGACCTGCTCCCGCGAATGATGTTGAC 1080
Qy
1081 CCCCCCGGAAGCGTGTGGATTCTCCCATGCTGAGCCGTCAACGGGAAGCGGACAGAG 1140
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Qy
1141 CGGAAGTCCATGGAAGTCTGAGCATCACCATGCGGGGTGGTGGCTCCCGTGTACCC 1200
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Db
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Qy
1381 AGCTGCTCTCTCGGGGGCCCCAGGGGTGGGGGCGCGGGGAGCAGCCCGCGCCCCAGT 1440
Db
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1441 GCCCGCTCCACACCCCTGCGCGCGCCCCCAGAGCTCCCGCGCTCTCTTGGGGGACCC 1500
Qy
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Db
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Db
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Qy
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Db
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Qy
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Db
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1861 AGTGTGCTCTACAGACAGCTTTCAGGGCCGAGTACAAGGCCAGTGGGGCCCTCCGTC 1920
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1861 AGTGTGCTCTACAGACAGCTTTCAGGGCCGAGTACAAGGCCAGTGGGGCCCTCCGTC 1920
Qy
1921 TTCCAAAAGCCGCTCCGCTTTCAGAGTGGAGCATAGTCTCTGAGGGTCCAGAGCCCTCC 1980
Db
1921 TTCCAAAAGCCGCTCCGCTTTCAGAGTGGAGCATAGTCTCTGAGGGTCCAGAGCCCTCC 1980
Qy
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Db
1981 CGCGAGCGGAGCGGAGCGAGTGTGGCATCTACTCCGTCACTTCACTCTCTCATCTCG 2040
Qy
2041 GGTCTCCAGACCGCTCGGTTCAAGCGAGTGTGGAGACCATCAGGCAAGCTCTCTGAGCACT 2100
Db
2041 GGTCTCCAGACCGCTCGGTTCAAGCGAGTGTGGAGACCATCAGGCAAGCTCTCTGAGCACT 2100
Qy
2101 CATGACAGCGCTCTCGTGCAGCGCTTCGAGAGGAGCAAGAGGAGGAGGAGGAGGAGG 2160
Db
2101 CATGACAGCGCTCTCGTGCAGCGCTTCGAGAGGAGCAAGAGGAGGAGGAGGAGGAGG 2160
Qy
2161 GCTGTGCCCCACCCCGAAGCTTCAGCGCCCGCCAGCCCGCGCGCCAGAGCTGAGC 2220
Db
2161 GCTGTGCCCCACCCCGAAGCTTCAGCGCCCGCCAGCCCGCGCGCCAGAGCTGAGC 2220
Qy
2221 AGCTCTCCCGCGAGCGCCCCCAAGGAGCAAGAGTCTCTGCGCCACCAACGAGGAGCCCT 2280
Db
2221 AGCTCTCCCGCGAGCGCCCCCAAGGAGCAAGAGTCTCTGCGCCACCAACGAGGAGCCCT 2280
Qy
2281 CTGCCCCGA 2289
Db
2281 CTGCCCCGA 2289

RESULT 2
US-10-116-326-5
; Sequence 5, Application US/10116326
; Patent No. 6777545
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: No. 6777545el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; PRIOR APPLICATION NUMBER: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036

;; PRIOR FILING DATE: 2001-04-06
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5
;; LENGTH: 2112
;; TYPE: DNA
;; ORGANISM: homo sapiens
US-10-116-326-5

Query Match 88.3%; Score 2020.2; DB 4; Length 2112;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	265	TTTAGGTACCTGGTCTCGGAGCAGCTCTCGGGGGTGCAGTATTCGACTACCTGGTAAAG	324
Db	88	TAATTTGACCTGGTCTCGGAGCAGCTCTCGGGGGTGCAGTATTCGACTACCTGGTAAAG	147
Qy	325	AAGGGAGAGACTGACGCCCAAGAGGGCCGAAAGTTCTTCGCCACAGATTTGTCTGCGCTG	384
Db	148	AAGGGAGAGACTGACGCCCAAGAGGGCCGAAAGTTCTTCGCCACAGATTTGTCTGCGCTG	207
Qy	385	GACTTCTGCCACAGTACTCCATCTGCCACAGACCTAAAGCCCGAGAACCTGTCTTTTG	444
Db	208	GACTTCTGCCACAGTACTCCATCTGCCACAGACCTAAAGCCCGAGAACCTGTCTTTTG	267
Qy	445	GATGAGAAAAACAATCCGATTTGCAGACTTCCGGCATGGGTCCCTTGCAGGTGGGGAC	504
Db	268	GATGAGAAAAACAATCCGATTTGCAGACTTCCGGCATGGGTCCCTTGCAGGTGGGGAC	327
Qy	505	AGCTCTCTGAGACCACTCGGGTCCCGCATTTATCGGTGTCAGAGGTGATTAAGGGG	564
Db	328	AGCTCTCTGAGACCACTCGGGTCCCGCATTTATCGGTGTCAGAGGTGATTAAGGGG	387
Qy	565	GAAAAATATGATGGCCCGCGGACAGATGTGAGTGTGAGTCACTCTTCGCCCTG	624
Db	388	GAAAAATATGATGGCCCGCGGACAGATGTGAGTGTGAGTCACTCTTCGCCCTG	447
Qy	625	CTCGTGGGGGCTTGCCCTTTGATGACGACAACTCCCGCAGCTGTGAGAGGTGAA	684
Db	448	CTCGTGGGGGCTTGCCCTTTGATGACGACAACTCCCGCAGCTGTGAGAGGTGAA	507
Qy	685	CGGGGCGTCTTCCACATGCCCACTTCACTTCTCCAGATTGCCAGAGCCCTCGTGGGGG	744
Db	508	CGGGGCGTCTTCCACATGCCCACTTCACTTCTCCAGATTGCCAGAGCCCTCGTGGGGG	567
Qy	745	ATGATCGAAGTGGAGCCGAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTTGG	804
Db	568	ATGATCGAAGTGGAGCCGAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTTGG	627
Qy	805	TACCTAGGCGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCGCGGGTA	864
Db	628	TACCTAGGCGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCGCGGGTA	687
Qy	865	GCCATGGGAGCTGCCATCCAGCGGAGCTGACCCCGACGCTCTAGAGAGCATGGCA	924
Db	688	GCCATGGGAGCTGCCATCCAGCGGAGCTGACCCCGACGCTCTAGAGAGCATGGCA	747
Qy	925	TCACTGGGCTGCTTTCAGGGACCGGAGAGGCTGCATCGCAGCTGCGCAGTGAGAGGAG	984
Db	748	TCACTGGGCTGCTTTCAGGGACCGGAGAGGCTGCATCGCAGCTGCGCAGTGAGAGGAG	807
Qy	985	AACCAAGAAAAGATGATATATTTATCTGTTTGGATCGGAAGGAGCGGTATCCAGCTGT	1044
Db	808	AACCAAGAAAAGATGATATATTTATCTGTTTGGATCGGAAGGAGCGGTATCCAGCTGT	867
Qy	1045	GAGACACGAGCTGCTCCCGGAATGATTTGACCCCGCCCGGAAAGCGGTGGAATCT	1104
Db	868	GAGACACGAGCTGCTCCCGGAATGATTTGACCCCGCCCGGAAAGCGGTGGAATCT	927
Qy	1105	CCCATGTGACCGCTACCGGAGCGGACCGAGCGGAGTCCATGGAAGTCTCTGAGC	1164
Db	928	CCCATGTGACCGCTACCGGAGCGGACCGAGCGGAGTCCATGGAAGTCTCTGAGC	987

Qy	1165	ATCACCGATGCCGGGGTGGTGGCTCCCTGTATCCCAACCGACGGGCTTGGAGATGGCC	1224
Db	988	ATCACCGATGCCGGGGTGGTGGCTCCCTGTATCCCAACCGACGGGCTTGGAGATGGCC	1047
Qy	1225	CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCTTCCACGGGTCTGTCTCCAGCCCT	1284
Db	1048	CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCTTCCACGGGTCTGTCTCCAGCCCT	1107
Qy	1285	CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTACCGAGCCGGGGCTGGAGATGAG	1344
Db	1108	CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTACCGAGCCGGGGCTGGAGATGAG	1167
Qy	1345	GCTCGAGCGGGGGCTCCCGACTTCCAAAAGCAGACGTGCTTCTCGGGGCCCCAGG	1404
Db	1168	GCTCGAGCGGGGGCTCCCGACTTCCAAAAGCAGACGTGCTTCTCGGGGCCCCAGG	1227
Qy	1405	GGTGGGGCGCCCGGGAGCAGACCCCGCCCGCCAGTCCCGCTCCACACCCCTCCCGGC	1464
Db	1228	GGTGGGGCGCCCGGGAGCAGACCCCGCCCGCCAGTCCCGCTCCACACCCCTCCCGGC	1287
Qy	1465	CCCCCAGGCTCCCGGCTCTCTGGGGGACCCCTTTGCACTCGCTCTTGCAACAGGCC	1524
Db	1288	CCCCCAGGCTCCCGGCTCTCTGGGGGACCCCTTTGCACTCGCTCTTGCAACAGGCC	1347
Qy	1525	CGGGCAGTCCCAACCGGGACCCCGGGGACCAACCCCGCCAGCCCGCGGGTGGGTC	1584
Db	1348	CGGGCAGTCCCAACCGGGACCCCGGGGACCAACCCCGCCAGCCCGCGGGTGGGTC	1407
Qy	1585	GGGGGAGCCCTTGGAGAGTCTGCTCAACTCCATCCGCAACAGCTTCTTGGGCTCCCT	1644
Db	1408	GGGGGAGCCCTTGGAGAGTCTGCTCAACTCCATCCGCAACAGCTTCTTGGGCTCCCT	1467
Qy	1645	CGCTTTTACCGGGCAGATGCAAGTCCCTTACCGCTCAGGAGATGTCCAGCTTCAAGCA	1704
Db	1468	CGCTTTTACCGGGCAGATGCAAGTCCCTTACCGCTCAGGAGATGTCCAGCTTCAAGCA	1527
Qy	1705	GAGTCTTCCCGGAGCTGGCAAAACGCTCTGTTTGGGAACTTCATCTCTTGGACAAA	1764
Db	1528	GAGTCTTCCCGGAGCTGGCAAAACGCTCTGTTTGGGAACTTCATCTCTTGGACAAA	1587
Qy	1765	GAAGAAACAATATTTCTCTGCTGCTAAAGGACAACTCTCAGCAGCATCAAGCAGACATC	1824
Db	1588	GAAGAAACAATATTTCTCTGCTTAAAGGACAACTCTCAGCAGCATCAAGCAGACATC	1647
Qy	1825	GTCCATGCTCTTCTGTGATCCCGCAGCTGAGTGCACAGTGTGTGTGCACAGCAGCTTC	1884
Db	1648	GTCCATGCTCTTCTGTGATCCCGCAGCTGAGTGCACAGTGTGTGTGCACAGCAGCTTC	1707
Qy	1885	AGGGCCGAGTACAAAGCCAGTGGGGCCCTTCCGTCTTCCAAAGCCCGTCCGCTTCAG	1944
Db	1708	AGGGCCGAGTACAAAGCCAGTGGGGCCCTTCCGTCTTCCAAAGCCCGTCCGCTTCAG	1767
Qy	1945	GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGACGGGACGGCAGCGAGGT	2004
Db	1768	GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGACGGGACGGCAGCGAGGT	1827
Qy	2005	GGTGGCATCTACTCCGTCAGCTTCACTCTCATCTCGGGTCCCGAGCCCTCGGTTCAAGCA	2064
Db	1828	GGTGGCATCTACTCCGTCAGCTTCACTCTCATCTCGGGTCCCGAGCCCTCGGTTCAAGCA	1887
Qy	2065	GTGGTGGAGACCATCCAGGACAGCTCTTGAGCACTCATGACAGCCCTCCGTCAGGCTC	2124
Db	1888	GTGGTGGAGACCATCCAGGACAGCTCTTGAGCACTCATGACAGCCCTCCGTCAGGCTC	1947
Qy	2125	CTGGCAGACGAGAAACGGGGCCAGACCCGGGCTGCTGGTGGCCCAACCCCGAGGCTG	2184
Db	1948	CTGGCAGACGAGAAACGGGGCCAGACCCGGGCTGCTGGTGGCCCAACCCCGAGGCTG	2007
Qy	2185	CAGCCCCCAGCCCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCCCCC	2244
Db	2008	CAGCCCCCAGCCCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCCCCC	2067
Qy	2245	AAGGACAAAGAGTCTCTGGGCCACCAACGGGACCCCTCTGCCCCCTGA	2289

Db	2068	AAGGACAAAGAGCTCTGGCCACCAACGGGACCCCTCTGCCCTGA	2112
RESULT 3			
US-10-116-326-1			
; Sequence 1, Application US/10116326			
; Patent No. 6777545			
; GENERAL INFORMATION:			
; APPLICANT: Turner, C. Alexander Jr.			
; APPLICANT: Mathur, Brian			
; APPLICANT: Friddle, Carl Johan			
; TITLE OF INVENTION: No. 6777545el Human Kinases and Polynucleotides Encoding the Same			
; FILE REFERENCE: LEX-0332-USA			
; CURRENT APPLICATION NUMBER: US/10/116,326			
; CURRENT FILING DATE: 2002-04-04			
; PRIOR APPLICATION NUMBER: US 60/282,036			
; PRIOR FILING DATE: 2001-04-06			
; NUMBER OF SEQ ID NOS: 6			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 2337			
; TYPE: DNA			
; ORGANISM: homo sapiens			
US-10-116-326-1			
Query Match 88.3%; Score 2020.2; DB 4; Length 2337;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy	265	TTTAGTACTGTTCTGAGACAGCTCTCGGGGGTGAGTATTGCACTACCTGGTAAAG	324
Db	313	TAATTGTACCTGTTCTGAGACAGCTCTCGGGGGTGAGCTATTGCACTACCTGGTAAAG	372
Qy	325	AAGGGAGACTGACGCGCCAGAGAGGCCGAAAGTTCTTCGCGCAGATTGTTGTCGCGCTG	384
Db	373	AAGGGAGACTGACGCGCCAGAGAGGCCGAAAGTTCTTCGCGCAGATTGTTGTCGCGCTG	432
Qy	385	GACTTCTGCCACAGCTACTCCATCTGCGCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG	444
Db	433	GACTTCTGCCACAGCTACTCCATCTGCGCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG	492
Qy	445	GATGAGAAAAACATCCGATTTGAGACTTTCGGGATGCGGTCCCTGCGAGGTGGGGAC	504
Db	493	GATGAGAAAAACATCCGATTTGAGACTTTCGGGATGCGGTCCCTGCGAGGTGGGGAC	552
Qy	505	AGCTCTCTGAGACCACTGCGGTCCCGCATTTATGCGGTCCAGAGGTGATTAAAGGG	564
Db	553	AGCTCTCTGAGACCACTGCGGTCCCGCATTTATGCGGTCCAGAGGTGATTAAAGGG	612
Qy	565	GAATAATATGATGGCCCGCGGAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTG	624
Db	613	GAATAATATGATGGCCCGCGGAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTG	672
Qy	625	CTGTGGGGCTTTCGCTTTGATGAGCAAACTTCGCGCAGCTGTGGAGAGGTGAAA	684
Db	673	CTGTGGGGCTTTCGCTTTGATGAGCAAACTTCGCGCAGCTGTGGAGAGGTGAAA	732
Qy	685	CGGGGCTCTTCCACATGCCCCCACTTCATTCCTCCAGATTGCCAGAGCTCTGAGGGGA	744
Db	733	CGGGGCTCTTTCACATGCCCCCACTTCATTCCTCCAGATTGCCAGAGCTCTGAGGGGA	792
Qy	745	ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGAGCAAAATTCAGAAACATCTTTGG	804
Db	793	ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGAGCAAAATTCAGAAACATCTTTGG	852
Qy	805	TACCTAGGGGGAAAAACAGAGCCAGACCCGCTGCTGAGCCAGCCCTCGCGCGGGTA	864
Db	853	TACCTAGGGGGAAAAACAGAGCCAGACCCGCTGCTGAGCCAGCCCTCGCGCGGGTA	912
Qy	865	GCCATCGGAGCTTCCATCCACGGAGAGCTGACCCCGACGCTCTAGAGAGCATGGCA	924
Db	913	GCCATCGGAGCTTCCATCCACGGAGAGCTGACCCCGACGCTCTAGAGAGCATGGCA	972

Qy	925	TCACTGGGCTGCTTTCAGGACCGCGAGAGGCTGCATCGGAGCTGCGCACTGAGGAGGAG	984
Db	973	TCACTGGGCTGCTTTCAGGACCGCGAGAGGCTGCATCGGAGCTGCGCACTGAGGAGGAG	1032
Qy	985	AACCAAGAAAAAGATGATATATATCTCTTTGGATCGGAGAGCGGTATCCAGCTGT	1044
Db	1033	AACCAAGAAAAAGATGATATATATCTCTTTGGATCGGAGAGCGGTATCCAGCTGT	1092
Qy	1045	GAGGACAGGACCTGCTCCCGGAATGATTTGACCCCGCCCGGAAGCGTGTGGATTCT	1104
Db	1093	GAGGACAGGACCTGCTCCCGGAATGATTTGACCCCGCCCGGAAGCGTGTGGATTCT	1152
Qy	1105	CCCATGCTGAGCCGTCAACGGGAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC	1164
Db	1153	CCCATGCTGAGCCGTCAACGGGAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC	1212
Qy	1165	ATCACCGATGCGGGGGTGGTGGCTCCCTGTATACCCACCGAGCGGCTTTGGAGATGGCC	1224
Db	1213	ATCACCGATGCGGGGGTGGTGGCTCCCTGTATACCCACCGAGCGGCTTTGGAGATGGCC	1272
Qy	1225	CAGCAGACGAGATCCCGTAGCGTCAGTGGAGCCTCCACGGGTCTGTCTCCAGGCCCT	1284
Db	1273	CAGCAGACGAGATCCCGTAGCGTCAGTGGAGCCTCCACGGGTCTGTCTCCAGGCCCT	1332
Qy	1285	CTAAGCAGCCCAAGGAGTCCGCTCTTTTCTTTTCAACCGGAGCCGGGGCTGGAGATGAG	1344
Db	1333	CTAAGCAGCCCAAGGAGTCCGCTCTTTTCTTTTCAACCGGAGCCGGGGCTGGAGATGAG	1392
Qy	1345	GCTCGAGGGGGGCTCCCGACTTCCAAACCGCAGACGCTCTCTCGGGGGCCCGAG	1404
Db	1393	GCTCGAGGGGGGCTCCCGACTTCCAAACCGCAGACGCTCTCTCGGGGGCCCGAG	1452
Qy	1405	GGTGGGGGGCGCGGGAGAGAGCCCGCGCCCGCCAGTGCCTCCACACCCCTCGCCGCG	1464
Db	1453	GGTGGGGGGCGCGGGAGAGAGCCCGCGCCCGCCAGTGCCTCCACACCCCTCGCCGCG	1512
Qy	1465	CCCCCAGGCTCCCGGGCTCTCTGCGGGGACCCCTTTGACCTGCGCTCTGCAACGCCCC	1524
Db	1513	CCCCCAGGCTCCCGGGCTCTCTGCGGGGACCCCTTTGACCTGCGCTCTGCAACGCCCC	1572
Qy	1525	CGGGCAGTCCCAACCGGGGACCAACACCCCGGAGCAACACCCCGCGGGTGGGGTC	1584
Db	1573	CGGGCAGTCCCAACCGGGGACCAACACCCCGGAGCAACACCCCGCGGGTGGGGTC	1632
Qy	1585	GGGGGAGCGCTTGGAGGAGTCTCTCAATCCATCGCAACAGCTTCTCGGGCTCCCT	1644
Db	1633	GGGGGAGCGCTTGGAGGAGTCTCTCAATCCATCGCAACAGCTTCTCGGGCTCCCT	1692
Qy	1645	CGCTTTCAACGGCGCAGATGAGTCCCTTACCGCTGAGGAGATGTCAGCTTGAACGCCA	1704
Db	1693	CGCTTTCAACGGCGCAGATGAGTCCCTTACCGCTGAGGAGATGTCAGCTTGAACGCCA	1752
Qy	1705	GAGTCTCTCCCGAGCTGGCAAAACGCTCTCTGTTTGGGAACTTCATCTCTTTGGACAAA	1764
Db	1753	GAGTCTCTCCCGAGCTGGCAAAACGCTCTCTGTTTGGGAACTTCATCTCTTTGGACAAA	1812
Qy	1765	GAAGAAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAAGCAGACATC	1824
Db	1813	GAAGAAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAAGCAGACATC	1872
Qy	1825	GTCCATGCTCTTCTGTCGATCCCGAGCTGAGTCAAGTGTGTCGTCACAGACAGCTTC	1884
Db	1873	GTCCATGCTCTTCTGTCGATCCCGAGCTGAGTCAAGTGTGTCGTCACAGACAGCTTC	1932
Qy	1885	AGGGCCGAGTACAAAGCCAGTGGGGCCCTCTCGTCTTCCAAAGCCCGCTTCAG	1944
Db	1933	AGGGCCGAGTACAAAGCCAGTGGGGCCCTCTCGTCTTCCAAAGCCCGCTTCAG	1992
Qy	1945	GTGGACATCAGCTCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGT	2004
Db	1993	GTGGACATCAGCTCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGT	2052

Qy 2005 GGTGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCGTTCGGTTCAAGCGA 2064
Db 2053 GGTGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCGTTCGGTTCAAGCGA 2112
Qy 2065 GTGTGGAGACCATCCAGGACAGCTCTGTAGCACTCATGACCAAGCCCTCCGTCAGGCC 2124
Db 2113 GTGTGGAGACCATCCAGGACAGCTCTGTAGCACTCATGACCAAGCCCTCCGTCAGGCC 2172
Qy 2125 CTGCGAGACGAGAAAGCGGGCCAGACCCCGGCTCTGTGTGCTGCCACCCCGAAGCTG 2184
Db 2173 CTGCGAGACGAGAAAGCGGGCCAGACCCCGGCTCTGTGTGCTGCCACCCCGAAGCTG 2232
Qy 2185 CAGCCCCACCCCGCCAGACCCAGAGCTGAGCAAGCTCTCCCGCGAGGCCCCGCC 2244
Db 2233 CAGCCCCACCCCGCCAGACCCAGAGCTGAGCAAGCTCTCCCGCGAGGCCCCGCC 2292
Qy 2245 AAGGACAAGAGCTCTTGGCCACCAAGCGGACCCCTCTTGCCTGA 2289
Db 2293 AAGGACAAGAGCTCTTGGCCACCAAGCGGACCCCTCTTGCCTGA 2337

RESULT 4
US-10-003-690-1
; Sequence 1, Application US/10003690
; Patent No. 6787345
; GENERAL INFORMATION:
; APPLICANT: RORY A.J. CURTIS
; TITLE OF INVENTION: 55053, A NO. 6787345el Human Eukaryotic Kinase
; FILE REFERENCE: MNI-206
; CURRENT APPLICATION NUMBER: US/10/003,690
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/248,893
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2980
; TYPE: DNA
; ORGANISM: Homo. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2419)
US-10-003-690-1

Query Match 88.3%; Score 2020.2; DB 4; Length 2980;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 265 TTTAGGTACTCTGGTTCTGGAGCAGCTCTCGGGGGTGAGCTATTGACTACCTGGTAAAG 324
Db 398 TATTGTACTCTGGTTCTGGAGCAGCTCTCGGGGGTGAGCTATTGACTACCTGGTAAAG 457
Qy 325 AAGGGGAGCTGACGCCCAAGAGGCCGGAAGTCTTCGCCAGATGTGTGCGCTG 384
Db 458 AAGGGGAGCTGACGCCCAAGAGGCCGGAAGTCTTCGCCAGATGTGTGCGCTG 517
Qy 385 GACTTCTGCCACAGCTACTCTCATCTGCCACAGAGACCTTAAAGCCCGAGAACCTCTTTTG 444
Db 518 GACTTCTGCCACAGCTACTCTCATCTGCCACAGAGACCTTAAAGCCCGAGAACCTCTTTTG 577
Qy 445 GATGAGAAAAAACAATCCGATTCGAGACTTCGGCATGGCTCCCTGCGAGGTGGGGAC 504
Db 578 GATGAGAAAAAACAATCCGATTCGAGACTTCGGCATGGCTCCCTGCGAGGTGGGGAC 637
Qy 505 AGCTCTCGAGACAGCTGCGGTGCCCCCAATTATGCGTGTCCAGAGGTGATTAAAGGG 564
Db 638 AGCTCTCGAGACAGCTGCGGTGCCCCCAATTATGCGTGTCCAGAGGTGATTAAAGGG 697
Qy 565 GAAAAATATGATGCGCCCGGCGAGACATGTGGAGCTGTGGAGTCATCTTTCGCCCTG 624
Db 698 GAAAAATATGATGCGCCCGGCGAGACATGTGGAGCTGTGGAGTCATCTTTCGCCCTG 757

Qy 625 CTGTCGGGGGCTCTGCCCCCTTTGATGACGACAACTCTCGCCAGCTGCTGGAGAAAGTGAAA 684
Db 758 CTGTCGGGGGCTCTGCCCCCTTTGATGACGACAACTCTCGCCAGCTGCTGGAGAAAGTGAAA 817
Qy 685 CGGGCGCTCTTCCACATGCCCCCACTTCAATTCCTCCAGATTGCCAGAGCTCTCAGAGGGA 744
Db 818 CGGGCGCTCTTCCACATGCCCCCACTTCAATTCCTCCAGATTGCCAGAGCTCTCAGAGGGA 877
Qy 745 ATGATCGAATGAGAGCCGGAATAAAGGCTCAGTCTGTGAGCAAAATTCAGAAACATCTTTGG 804
Db 878 ATGATCGAATGAGAGCCGGAATAAAGGCTCAGTCTGTGAGCAAAATTCAGAAACATCTTTGG 937
Qy 805 TACTTAGCGGGGAAAACACAGAGCCAGACCCGCTGCTGAGCCAGCCCTGCGCGCGGGTA 864
Db 938 TACTTAGCGGGGAAAACACAGAGCCAGACCCGCTGCTGAGCCAGCCCTGCGCGCGGGTA 997
Qy 865 GCCATGCGGAGCCCTGCCATCCAAACGAGAGCTGAGACCCCGACGCTCTAGAGAGCATGGCA 924
Db 998 GCCATGCGGAGCCCTGCCATCCAAACGAGAGCTGAGACCCCGACGCTCTAGAGAGCATGGCA 1057
Qy 925 TCACTGGGCTGCTTCAGGGACCCGAGAGGCTGCATCCGAGCTGCGCAGTGTGAGAGGAG 984
Db 1058 TCACTGGGCTGCTTCAGGGACCCGAGAGGCTGCATCCGAGCTGCGCAGTGTGAGAGGAG 1117
Qy 985 AACCAAGAAAAGATGATATATATCTCTTTTGGATCGGAAGAGCGGTATCCCAAGCTGT 1044
Db 1118 AACCAAGAAAAGATGATATATATCTCTTTTGGATCGGAAGAGCGGTATCCCAAGCTGT 1177
Qy 1045 GAGGACCAAGACCTGCTCCCGGAATGATGTTGACCCCGGGAAGCGGTGTGATTTCT 1104
Db 1178 GAGGACCAAGACCTGCTCCCGGAATGATGTTGACCCCGGGAAGCGGTGTGATTTCT 1237
Qy 1105 CCATGCTGAGCCGTCAACGGGAAGCGCGACGAGCGGAAGTCCATGGAAGTCTCTGAGC 1164
Db 1238 CCATGCTGAGCCGTCAACGGGAAGCGCGACGAGCGGAAGTCCATGGAAGTCTCTGAGC 1297
Qy 1165 ATCAACGATCCGGGGGTGTGCTCCCTGTATCCACCGAGCGGGCTTGGAGATGGCC 1224
Db 1298 ATCAACGATCCGGGGGTGTGCTCCCTGTATCCACCGAGCGGGCTTGGAGATGGCC 1357
Qy 1225 CAGCAGACGAGAGATCCCTAGCTGAGTGGAGCTTCCAGGGTCTGCTCTCCAGCCCT 1284
Db 1358 CAGCAGACGAGAGATCCCTAGCTGAGTGGAGCTTCCAGGGTCTGCTCTCCAGCCCT 1417
Qy 1285 CTAAAGAGCCCAAGAGTCCGGTCTTTTCTTTTCAACGGAGCGCGGGGCTGGAGATGAG 1344
Db 1418 CTAAAGAGCCCAAGAGTCCGGTCTTTTCTTTTCAACGGAGCGCGGGGCTGGAGATGAG 1477
Qy 1345 GCTCGAGCGGGGCTCTCCCGACTTCCAAAACGAGAGCTGCTTCTCGGGGCCCCCAGG 1404
Db 1478 GCTCGAGCGGGGCTCTCCCGACTTCCAAAACGAGAGCTGCTTCTCGGGGCCCCCAGG 1537
Qy 1405 GGTGGGGGCGCGGGGAGAGCCCGCCCGCCAGTCCCGCTCCACACCCCTGCCCGGC 1464
Db 1538 GGTGGGGGCGCGGGGAGAGCCCGCCCGCCAGTCCCGCTCCACACCCCTGCCCGGC 1597
Qy 1465 CCCCCAGGCTCCCCCGGCTCTCTGCGGAGACCCCTTGCACCTGCTGTCACACGCCC 1524
Db 1598 CCCCCAGGCTCCCCCGGCTCTCTGCGGAGACCCCTTGCACCTGCTGTCACACGCCC 1657
Qy 1525 CGGGCCAGTCCCAACCGGGACCCCGGGGACAAACACACCCCGCCAGCCCGCGGTGGCGTC 1584
Db 1658 CGGGCCAGTCCCAACCGGGACCCCGGGGACAAACACACCCCGCCAGCCCGCGGTGGCGTC 1717
Qy 1585 GGGGAGCCCGCTGGAGGAGTCTCTCAATCCATCCGACAGCTTCTGGGCTCCGCT 1644
Db 1718 GGGGAGCCCGCTGGAGGAGTCTCTCAATCCATCCGACAGCTTCTGGGCTCCGCT 1777
Qy 1645 CGCTTTTCAACCGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCCAGCTTTCAGCCCA 1704
Db 1778 CGCTTTTCAACCGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCCAGCTTTCAGCCCA 1837
Qy 1705 GAGTCTCTCCCGGAGCTGGCAAAAACGCTCTCTGGTTTCGGGAACCTTTCATCTCTCTTGGACAAA 1764

Db 1453 GGTGGGGCGCGGGGAGCAGCCCCCGCCCCCAGTGCCCGCTCCACACCCCTGCCCGG 1512
Qy 1465 CCCCAGAGCTCCCGCGCTCTCTGGGGGAGACCCCTTGGACTGCGCTTGCAACAGCC 1524
Db 1513 CCCCAGAGCTCCCGCGCTCTCTGGGGGAGACCCCTTGGACTGCGCTTGCAACAGCC 1572
Qy 1525 CGGGCAGTCCACCGGGACCCCGGGGACACACCCCGGGGAGGCGGTC 1584
Db 1573 CGGGCAGTCCACCGGGACCCCGGGGACACACCCCGGGGAGGCGGTC 1632
Qy 1585 GGGGAGCGCGCTGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTGGGTCACCT 1644
Db 1633 GGGGAGCGCGCTGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTGGGTCACCT 1692
Qy 1645 CGTTTTCACCGGCGAGATGAGTCCCTTAAGGACAACTCTCAGCAGATGTCAGTTGACCCA 1704
Db 1693 CGTTTTCACCGGCGAGATGAGTCCCTTAAGGACAACTCTCAGCAGATGTCAGTTGACCCA 1752
Qy 1705 GAGTCTCCCGGAGCTGGCAAAAGCTCTCTGGTTCGGGAATTCATCTCTTGGACAAA 1764
Db 1753 GAGTCTCCCGGAGCTGGCAAAAGCTCTCTGGTTCGGGAATTCATCTCTTGGACAAA 1812
Qy 1765 GAAGAAACAATATTCCTCTGCTTAAGGACAACTCTCAGCAGATCAAAAGCAGATC 1824
Db 1813 GAAGAAACAATATTCCTCTGCTTAAGGACAACTCTCAGCAGATCAAAAGCAGATC 1872
Qy 1825 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCAAGTGTGTGTCAAGCAGCTTC 1884
Db 1873 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCAAGTGTGTGTCAAGCAGCTTC 1932
Qy 1885 AGGCGGAGTACAGGCGAGTGGGGCCCTCTCGTCTTCCAAAGCCGTCGCTTCAG 1944
Db 1933 AGGCGGAGTACAGGCGAGTGGGGCCCTCTCGTCTTCCAAAGCCGTCGCTTCAG 1992
Qy 1945 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGCGGAGCGGAGGT 2004
Db 1993 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGCGGAGCGGAGGT 2052
Qy 2005 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGTCCAGCCGTCGTTCAAGCGA 2064
Db 2053 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGTCCAGCCGTCGTTCAAGCGA 2112
Qy 2065 GTGTGAGACCATCCAGGACAGCTCTGAGCACTCATGACAGCCCTCGTGCAGGCC 2124
Db 2113 GTGTGAGACCATCCAGGACAGCTCTGAGCACTCATGACAGCCCTCGTGCAGGCC 2172
Qy 2125 CTGCGACAGGAGAAACGGGGCCAGACCGGGCTGTGTGTGCGCCACCCCGAGCGTG 2184
Db 2173 CTGCGACAGGAGAAACGGGGCCAGACCGGGCTGTGTGTGCGCCACCCCGAGCGTG 2232
Qy 2185 CAGCCCCCAGCGGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGGAGGCCCGCCC 2244
Db 2233 CAGCCCCCAGCGGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGGAGGCCCGCCC 2292
Qy 2245 AAGGACAGAGTCTTGGGCCACCAAGCGGACCCCTCTGCCC 2286
Db 2293 AAGGACAGAGTCTTGGGCCACCAAGCGGACCCCTCTGCCC 2334

RESULT 6

US-09-774-528-221
; Sequence 221, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong

; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774, 528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 221
; LENGTH: 1797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(1787)
US-09-774-528-221

Query Match 42.8%; Score 980; DB 4; Length 1797;
Best Local Similarity 75.4%; Pred. No. 1.2e-227;
Matches 1470; Conservative 0; Mismatches 0; Indels 480; Gaps 1;

Qy 268 AGGTACCTGTTCTGGAGCAGCTCTCGGGGGTGAAGTATTCGACTACCTGTTAAAGAG 327
Db 87 AGGTACCTGTTCTGGAGCAGCTCTCGGGGGTGAAGTATTCGACTACCTGTTAAAGAG 146
Qy 328 GGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGSCCAGATTGTCTGCGCTGGAC 387
Db 147 GGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGSCCAGATTGTCTGCGCTGGAC 206
Qy 388 TTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTCTGTTTGGAT 447
Db 207 TTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTCTGTTTGGAT 266
Qy 448 GAGAAAAACAATCCGCATTTGCAGATTGGCATGGCGTCCCTGCGAGGTGGGGACAGC 507
Db 267 GAGAAAAACAATCCGCATTTGCAGATTGGCATGGCGTCCCTGCGAGGTGGGGACAGC 326
Qy 508 CTCTCGAGAGCCAGCTCGGGGTCCCGCCATTTATCGGTGTCCAGAGGTGATTAAAGGGGAA 567
Db 327 CTCTCGAGAGCCAGCTCGGGGTCCCGCCATTTATCGGTGTCCAGAGGTGATTAAAGGGGAA 386
Qy 568 AAATATGATGCGCCCGGCGAGACATGTGAGCTGTGAGTGTATCTTCCGCTCTGCTC 627
Db 387 AAATATGATGCGCCCGGCGAGACATGTGAGCTGTGAGTGTATCTTCCGCTCTGCTC 446
Qy 628 GTGGGGCTCTGCGCTTTGATGACGACAACTCCCGCAGCTGTGGAGAGGTGAAACGG 687
Db 447 GTGGGGCTCTGCGCTTTGATGACGACAACTCCCGCAGCTGTGGAGAGGTGAAACGG 506
Qy 688 GCGCTCTTCACATGCCCCCACTTCATCTCCAGATTGCCAGAGCTCTGAGGGGATG 747
Db 507 GCGCTCTTCACATGCCCCCACTTCATCTCCAGATTGCCAGAGCTCTGAGGGGATG 566
Qy 748 ATCGAAGTGGAGCCGAAAGAGGCTCAGTCTGAGCAAAATTCAGAAACATCTTGGTAC 807
Db 567 ATCGAAGTGGAGCCGAAAGAGGCTCAGTCTGAGCAAAATTCAGAAACATCTTGGTAC 626
Qy 808 CTAGCGGGAAACACGAGCCAGACCCGCTGTGCTGAGGCGAGCCCTTGGCCCGGGTAGCC 867
Db 627 CTAGCGGGAAACACGAGCCAGACCCGCTGTGCTGAGGCGAGCCCTTGGCCCGGGTAGCC 686
Qy 868 ATGCGGAGCTTCCATCCACGAGAGCTGACCCCGACGCTCTAGAGAGCATGCGATCA 927
Db 687 ATGCGGAGCTTCCATCCACGAGAGCTGACCCCGACGCTCTAGAGAGCATGCGATCA 746
Qy 928 CTGGGCTGCTTTCAGGGACCGGAGAGGCTGATCGCGAGCTGCGCAGTGAGAGAGAAC 987
Db 747 CTGGGCTGCTTTCAGGGACCGGAGAGGCTGATCGCGAGCTGCGCAGTGAGAGAGAAC 806

QY 988 CAGAAAAGATATATATCTGCTTTTGGATCGAAGAGCGGTATCCAGCTGTGAG 1047
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QY 807 CAGAAAAGATATATATCTGCTTTTGGATCGAAGAGCGGTATCCAGCTGTGAG 866
DB |||||||
QY 1048 GACCAGACCTGCTCCCGGAATGATTTGACCCCGCCCGGAAGCGGTGTGGATTTCTCC 1107
DB |||||||
QY 867 GACCAGACCTGCTCCCGGAATGATTTGACCCCGCCCGGAAGCGGTGTGGATTTCTCC 926
DB |||||||
QY 1108 ATGCTGAGCCGTACCGGAAGCGGCACGAGCGGAAGTCCATGGAAGTCCCTGAGCATC 1167
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QY 927 ATGCTGAGCCGTACCGGAAGCGGCACGAGCGGAAGTCCATGGAAGTCCCTGAGCATC 986
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QY 1168 ACCGATCCCGGGGTGTGCTCCCTGTATCCACCGACCGCGCTTGAGATGGCCCGAG 1227
DB |||||||
QY 987 ACCGATCCCGGGGTGTGCTCCCTGTATCCACCGACCGCGCTTGAGATGGCCCGAG 1046
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QY 1228 CACAGCCAGAGATCCCGTAGCGTCACTGAGGACCTCCACGCGGTCTGCTCCAGCCCTCTA 1287
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QY 1047 CACAGCCAGAG----- 1057
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DB |||||||
QY 1058 ----- 1057
DB |||||||
QY 1348 CGAGCGGGGCTCCCGACTTCCAAAACGACAGCTGCTTTCTCGGGGCCCGAGGGGT 1407
DB |||||||
QY 1058 ----- 1057
DB |||||||
QY 1408 GGGGCGCGGGGAGAGAGCCCCCGCCCGACAGTCCCGCTCCACACCCCTGCGCGGCC 1467
DB |||||||
QY 1058 ----- 1057
DB |||||||
QY 1468 CCAGGCTCCCGCGCTCTCTGGGGGACCCCTTTGCACTCGCTCTGACACGCCCGG 1527
DB |||||||
QY 1058 ----- 1057
DB |||||||
QY 1528 GCCAGTCCACCGGAGCCCGGGGACAAACACACCCCGGCGGCGGTGGCGTGGG 1587
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QY 1058 ----- 1057
DB |||||||
QY 1588 GGAGCGCGCTGGAGGAGTGTCTCACTCATCCGACACAGCTTCCTGGGCTCCCTCGC 1647
DB |||||||
QY 1058 ----- 1057
DB |||||||
QY 1648 TTTACCGGCGAAGATGACGCTCCCTACCGTGGAGGAGTGTCCAGCTTGACGCCAGAG 1707
DB |||||||
QY 1058 ----- 1057
DB |||||||
QY 1708 TCCTCCCGGAGCTGGCAAAACGCTCTGTGGTTCGGGAACTTCATCTCTTGGACAAAGAA 1767
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QY 1058 -----GCTGGCAAAACGCTCTGTGGTTCGGGAACTTCATCTCTTGGACAAAGAA 1106
DB |||||||
QY 1768 GAACAATATTTCTGCTTAAGGACAAACCTCTCAGCAGCATCAAGCAGACATCGTC 1827
DB |||||||
QY 1107 GAACAATATTTCTGCTTAAGGACAAACCTCTCAGCAGCATCAAGCAGACATCGTC 1166
DB |||||||
QY 1828 CATGCTTTCTGCTGATCCCGAGCTGAGTCACTGCTGCTGTCTCAGCAGCATCAAGCAGCTTCAGG 1887
DB |||||||
QY 1167 CATGCTTTCTGCTGATCCCGAGCTGAGTCACTGCTGCTGTCTCAGCAGCATCAAGCAGCTTCAGG 1226
DB |||||||
QY 1888 GCCGAGTACAAAGGCGAGTGGGGCCCTTCGCTTTTCCAAAAGCCCGTCCGCTTCAGGTG 1947
DB |||||||
QY 1227 GCCGAGTACAAAGGCGAGTGGGGCCCTTCGCTTTTCCAAAAGCCCGTCCGCTTCAGGTG 1286
DB |||||||
QY 1948 GACATCAGTCTCTGAGGCTCCAGAGCCCTCCCGGACGCGGAGCGGAGGTGGT 2007
DB |||||||
QY 1287 GACATCAGTCTCTGAGGCTCCAGAGCCCTCCCGGACGCGGAGCGGAGGTGGT 1346
DB |||||||
QY 2008 GGCATCTACTCGGTTCACCTTCACTCTCATCTCGGTTCAGCGCTCGGTTCAGCGAGTG 2067
DB |||||||
QY 1347 GGCATCTACTCGGTTCACCTTCACTCTCATCTCGGTTCAGCGCTCGGTTCAGCGAGTG 1406
DB |||||||
QY 2068 GTGGAGACCATCCAGGACAGCTCTGTAGCACTCATGACACGCCCTCCGTCGAGGCCCTG 2127
DB |||||||

DB 1407 GTGGAGACCATCCAGGACAGCTCTGTAGCACTCATGACCACTCCGTGAGGCCCTG 1466
QY |||||||
DB 2128 GCAGACGAGAAACCGGGCCAGACCCGGCTGTGTGGTGGCCACCCCGAAGACCTGCGAG 2187
DB |||||||
DB 1467 GCAGACGAGAAACCGGGCCAGACCCGGCTGTGTGGTGGCCACCCCGAAGACCTGCGAG 1526
QY |||||||
DB 2188 CCCCCACCCCGCGCCCGCCAGACCCAGAGCTG 2217
DB |||||||
DB 1527 CCCCCACCCCGCGCCCGCCAGACCCAGAGCTG 1556
QY |||||||

RESULT 7
US-09-930-181-3
; Sequence 3, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (482)...(2239)
US-09-930-181-3

Query Match 34.1%; Score 780.4; DB 3; Length 3364;
Best Local Similarity 68.0%; Pred. No. 3.6e-179;
Matches 1279; Conservative 0; Mismatches 406; Indels 195; Gaps 6;

QY 265 TTTAGGTACTGTTCTTGAGACGCTCTCGGGGGTGTGAGCTATTCGACTACCTGTTAAAG 324
DB |||||||
DB 500 TGTAGGTACTGTTCTTGAGAACGCTGTCAAGTGTGTGAGCTCTTCGACTACCTGTTGAAG 559
QY |||||||
DB 325 AAGGGAGACTGACGCGCCCAAGGAGGCCGAAAGTCTTCGCCGACAGATTTGTCTGCGCTG 384
DB |||||||
DB 560 AAGGGAGGCTGACGCGCTAAGAGGCTCGGAAGTCTTCGCCGACATCATCTGCGCTG 619
QY |||||||
DB 385 GACTCTTGCCACAGCTACTCCATCTGCCACAGAGACTTAAAGCCCGAGAACCTGCTTTTG 444
DB |||||||
DB 620 GACTCTTGCCACAGCTACTCCATATGACACAGGATCTGAAACCTGAAACCTCTCTGCTG 679
QY |||||||
DB 445 GATGAGAAACAAACATCCCGCATTTGAGACTTCGGCATGGCGTCCCTGCGAGTGGGGAC 504
DB |||||||
DB 680 GACGAGAAACAAACATCCCGCATTCGAGACTTTTGGCATGGCGTCCCTGCGAGTTGGCGAC 739
QY |||||||
DB 505 AGCTCTCTGAGACCACTGCGGTCCCGCATTTATGCTGTCTCCAGAGTGAATTAAGGGG 564
DB |||||||
DB 740 AGCTCTTGAGACCACTGTTGGTCCCGCATCTACGCTGCGCCGAGGTGATCCGGGG 799
QY |||||||
DB 565 GAAAAATATGATGAGCCCGCGGACAGATGTGAGCTGTGAGTATCTCTTCGCGCTG 624
DB |||||||
DB 800 GAGAAGTATGACGCGCCGGAAGGAGCGTGTGAGCTGCGGCGTCTATCTGTTCCGCTTG 859
QY |||||||
DB 625 CTGTTGGGGCTCTGCGCTTTGATGACAGCAACCTCCCGCAGCTGCTGGAGAGTGAAG 684
DB |||||||
DB 860 CTGTTGGGGCTCTGCGCTTTGAGATGACAACTTTGAGACAGCTGTGAGAGGTGAG 919
QY |||||||
DB 685 CGGGCGCTCTTCCACATGCGCCCACTTCAITTCCTCCAGATTGCCAGAGCTCTCTGAGGGGA 744
DB |||||||
DB 920 CGGGCGCTGTTCACATGCGCCCACTTTATCCGCGCCGACTGCCAGAGTCTCTACGGGGC 979
QY |||||||
DB 745 ATGATCGAAGTGTGAGCGCCGAAAAAGGCTGAGTGTGAGCAAAATTCAGAAACATCTTGG 804
DB |||||||
DB 980 ATGATCGAAGTGTGAGCGCGCGCAACGCGGCTCTACGCTAGAGCAATTCAGAAACATATGG 1039
QY |||||||

Qy	805	TACCTAGCGGGAAAACACAGAGCCAGACCCCGTGCCTGGAGCCAGCCCTGCGCGCGGGTA	864
Db	1040	TATATAGGGGCAAGATGAGCCCGAACC-----AGAGCAGCCCATTCCTCGCAAGGTG	1093
Qy	865	GCCATCGGGAGCCTGCCATCCACCGGAGAGCTGGACCCCGACCTCTTAGAGACATGGCA	924
Db	1094	CAGATCCGCTCGCTGCCACGCTTGGAGGACATCGACCCCGACGTCTGGACACGATGCAC	1153
Qy	925	TCACCTGGCTGCTTCAGGGACCGCGAGAGCTGCATCGCGAGCTGCGCAGTGAAGAGGAG	984
Db	1154	TCACCTGGCTGCTTCGAGACCGCAACAGCTGCTGCAGACCTGTGTCTCGAGAGGAG	1213
Qy	985	AACCAAGAAAGATGATATATTCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT	1044
Db	1214	AACCGAGAGAGATGATTATTCTCTCTCTCGACCGGAAAGAAAGGTATCCGAGCCAG	1273
Qy	1045	GAGGACAGAGACCTGCTCCCGCGAATGATTGACCCCGGAGAGCGTGTGGATTCT	1104
Db	1274	GAGGATGAGACCTGCCCCCGGAACGAGATAGACCTCTCCCGGAAGCGTGTGGACTCC	1333
Qy	1105	CCCATGCTGAGCCGTCAACGGGAAGCGGCGACCAAGAGCGGAAGTCCATGGAAGTCTTGAGC	1164
Db	1334	CCGATGCTGAACCGGCACGCAAGCGCGCGCAGAACGCAATCCATGAGAGGTCTCAGC	1393
Qy	1165	ATCACCGATGCGCGGGGTGTGTGCTCCCTGTATCCACCCGACGCGGCTTTGGAGATGGCC	1224
Db	1394	GTGACGACGCG-----GGCTCCCGGTGCTCGCGCGGGGCCATTGAGATGGCC	1444
Qy	1225	CAGCACAGCAGAGATCCCGTAGGTCAGTGGAGCCTCAGCGGTCTGTCTCTCCAGCCCT	1284
Db	1445	CAGCACGGCCAGAGGTCGTGGTCCATCAGCGGTGCTCTCTCAGGCTTTTCCACGAGCCCA	1504
Qy	1285	CTAAGCAGCCCAAGGAGTCCGGTCTTTCTTTTACCGGAGCGGGGCTGGAGATGAG	1344
Db	1505	CTCAGCAGCCCCCG-----	1518
Qy	1345	GCTCGAGCGCGGGGCTCCCCGACTTCCAAAACGCGAGACGTGCTCTCGGGGCCCCAGG	1404
Db	1519	-----	1518
Qy	1405	GTTGGGGGCGCGGGGAGCAGCCCCCGCCAGTCGCGCTCCACACCCCTGCCCGGC	1464
Db	1519	-----GGTGACCCCTCAACCCCTCACCAAGGGGCGAGTCCCTCCCTCCCG-----	1558
Qy	1465	CCCCCAGGCTCCCGCGCTCTCTTGGGGGACCCCTTGCACTGCTCTGTGCACACGCCC	1524
Db	1559	-----ACCCCCAAGGGGACACTGTGTCCACGCGCA	1588
Qy	1525	CGGGCCAGTCCCAACCGGGAACCCCGGGAACAACACCCCGACCCCGCGGCTGGCGTC	1584
Db	1589	AAGGAGAGCCGGCTGGCAGCCCAACCCCAACCCCGCGCTCCAGCCCG-----AGCGTC	1642
Qy	1585	GGGGGACCGCTGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTCTGGGTCCCTT	1644
Db	1643	GGAGGGGTGCTCTGGAGGGCGCGCTCAACTCCATCAAGAACAGCTTCTTGGGCTCACCC	1702
Qy	1645	CGCTTTCACCGGGCAAGATGACGCTCCCTACCGCTCAGGAGATGTCCAGCTTGAAGCCCA	1704
Db	1703	CGCTTTCACCGCGGAAACTGCAAGTTCCGAGCGCGGAGGAGATGTCCAACTGTGACACCA	1762
Qy	1705	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGTTTGGGAACTTCTCTCTTTGGACAAA	1764
Db	1763	GAGTCTGTCCTCGAGCTGGCGAAGAGTCTCTGTTTGGGAACTTTCATCAGCCTGGAGAAG	1822
Qy	1765	GAGGAACAAATATTCCTGTGCTTAAAGGACAAACCTCTCAGAGAGCATCAAGACGATC	1824
Db	1823	GAGGAGCAGATCTTCGTGGTGCATCAAAAGACAAACCTCTGAGCTCCATCAAGGCTGACATC	1882
Qy	1825	GTCCATGCTTTCTGTGATCCCGAGCTTGAGTCAACAGTGTGTCTCACAGACCGAGCTTC	1884
Db	1883	GTGCACGCTTCTGTGTGATTCACAGTCTAGGCACAGCGTCACTCTCCAAACGAGGCTTC	1942
Qy	1885	AGGGCCGAGTACAAGGGCCAGTGGCGGGCCCTCTCGTCTTTCCAAAAGCCGCTCCGCTCCAG	1944

[illegible]

Qy	511	CTGAGACACAGCTGGGGTCCCCCATTTATGGGTCTCAGAGGTGATTAAGGGGGA AAAA	570
Db	517	CTGACACCTTTCTGTGGCAGTCCCCCTTATGTGTCGCCAGAACTCTTCAGGGCA AAAAA	576
Qy	571	TATGATGGCCGCGGGCAGACATGTGGAGCTGTGGAGTCATCCTTCTGCGCCTGCTCGT	630
Db	577	TATGATGACCCGAGGTGGATGTGTGGAGCCTAGGAGTTATCCTCTATACATGGTGACG	636
Qy	631	GGGGCTCTGCCCTTTGATGACGACAAACCTCGCCACGCTGCTGGAGAGGTGAAAACGGGCG	690
Db	637	GGATCCCTGCCTTTTGATGGACAGAACCTCAAGGAGCTCGGGACGGGTACTGAGGGGA	696
Qy	691	GTCCTTCACATGCCCACTTCAATTCCTCAGATTGCCAGAGCCTCTGAGGGGAATGATC	750
Db	697	AAATACCGTATTTCATTTCTACATGTCCACGGGACTGTGAAAACCTGCTTTAAGAAAATTTCTC	756
Qy	751	GAAGTGGAGCCGAAAAAAGGCTCAGTCTGGAGCNAATTCAGAACATCCTTTGGTACCTA	810
Db	757	ATTCTTAAATCCAGCAGAGAGGGCACTTTAGAGCAAAATCATGNAAGATCGATGGATGAAT	816
Qy	811	G-----GCGGAAACACGACGACAGCCCGTCCCTGGAGGCACAGCCCTCGCGCGGGTA	864
Db	817	GTGGGTCAAGAAGATGATGAACCTAAAGCCTTACGTGGAGCCACTCCCTGACTACAAGGAC	876
Qy	865	GCCATGCGGA	874
Db	877	CCCGGGGA	886

RESULT 10

```

RES001 10
US-09-949-016-2385
; Sequence 2385, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL0011307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2385
; LENGTH: 2224
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2385

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Query Match	8.7%	Score 199.2;	DB 4;	Length 2224;
Best Local Similarity	59.2%	Pred. No. 2.3e-38;		
Matches 361;	Conservative	0;	Mismatches 243;	Indels 66;
				Gaps 1;

271	Qy	TACCTGGTTCTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAGAAAGGGG	330
272			
273			
274			
275			
276			
277	Db	TACCTTGTTCATGGAGTACGCTAGTTCGCGGAGAGGTATTTTGATTACCTAGTGGCTCATGGC	336
278			
279			
280			
281			
282			
283			
284			
285			
286			
287			
288			
289			
290	Qy	AGACTGACCCCAAGGAGGCCGGAAGTTCCTCCGCCAGATTGTGCTCTGCCTTGACATTC	390
291			
292			
293			
294			
295			
296			
297			
298			
299			
300	Db	AGGATGAAAGAAAAAGAGGCTCGAGCCAAAATTCGCCCAGATAGTGTCTGCTGTGCAGTAC	396
301			
302			
303			
304			
305			
306			
307			
308			
309			
310	Qy	TGCCACAGCTACTCCATCTGCCACAGAGACCTTAAAGCCCGAGAACTGCTTTTGGATGAG	450
311			
312			
313			
314			
315			
316			
317			
318			
319			
320	Db	TGTCACCAGAGTTATTGTGTCATAGAGACTTAAAGGCAGAAAACTGCTCTTGGATGCT	456
321			
322			
323			
324			
325			
326			
327			
328			
329			
330	Qy	AAAAACAACATCCGCAATTGCGACACTTCGGCATATGGCGTCCCTCGAGGTGGGGGACAGCTTC	510
331			
332			
333			
334			
335			
336			
337			
338			
339			
340	Db	GATATGAACATCAAGATTGCGACATTTGGCTTCAGCAATGAATTCACCTTTGGGAACAAG	516

Qy	511	CTGAGACACGCTCGGGTCCCCCATTTATCGCTGTCCAGAGGTGATTAAAGGGGAAAAA	570
Db	517	CTGACACCTTCTGTGGCAGTCCCCCTTATGCTGCCAGAACTCTTCAGGGCAAAAA	576
Qy	571	TATGATGCCGCGGGGAGACATGTGGAGCTGTGGAGTCATCTCTTCGCCCTGCTCGTG	630
Db	577	TATGATGGAACCGAGGTGGATGTGTGGAGCCTAGAGTTATCTCTATACACTGCTCAGC	636
Qy	631	GGGGCTCTGCCCTTTGATGACGACAACCTCCGCCAGCTGTGGAGAAAGTGAAACGGGCG	690
Db	637	GGATCCCTGCTTTTGATGGACAGAACCTCAAGGAGCTGCGGGAACGGGTACTGAGGGGA	696
Qy	691	GTCCTTCACATGCCCCCATCTTCCTCCAGATTGCCAGAGCCTCTGAGGGGAATGATC	750
Db	697	AAATACGGTATTCCATTCTCATGTCCACGGACTGTGAAAACCTGCTTTAAGAAATTTCTC	756
Qy	751	GAAGTGGAGCCCGAAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTCTGGTACCTA	810
Db	757	ATTCCTTAATCCCAAGCAAGAGGACATTTAGAGCAAAATCATGAAAGATCGATGGATGAAT	816
Qy	811	G-----GCGGGAAACAGAGCCAGACCCGCTGCTGGAGCCAGGCCCTCGGCCCGGGGTA	864
Db	817	GTGGGTCAACGAGATGATGAACCTAAAGCCTTACGTGGAGCCACTCCCTGACTACAAGGAC	876
Qy	865	GCCATGCGGA	874
Db	877	CCCCGGCGGA	886

RESULT 11

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RESULT 11
US-09-949-016-1546
; Sequence 1546, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1546
; LENGTH: 2950
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1546

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Query Match	8.7%	Score 199.2;	DB 4;	Length 2950;
Best Local Similarity	59.2%	Pred. No. 2.6e-38;		
Matches 361; Conservative	0;	Mismatches 243;	Indels 6;	Gaps 1;

Qy	271	TACCTGGTTCTGGAGCAGCTCTCGGGGGGTGAGCTATTCCGACTACCTGGTAAAGAAAGGGG	330
Db	684	TACCTTGTATGGAGTACGCTAGTGGCGGAGAGGTATTGATTACCTAGTGGCTCATGGC	743
Qy	331	AGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGCGCAGATTGTGTCGTGCGCTGGACTTC	390
Db	744	AGGATGAAGAAAAGAGGGCTCGAGCAAAATTCGCCCAGATAGTGTCTGCTGTGCAGTAC	803
Qy	391	TGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGGCCGAGAACCTGCTTTTGGATGAG	450
Db	804	TGTCAACAGAAATTATTGTGCCATAGAGACTTAAAGGCAGAAAAACCTGCTCTTGGATGCT	863
Qy	451	AAAAACAACATCCGCATTGCGAGACTTCGGGCATGGCGTCCCTGCAGGTGGGGGACAGCCTC	510

Db 864 GATATGAACATCAAGATTGCAGACTTTGGCTTCAGCAATGAATTCACCTTTTGGGAACAAG 923
QY 511 CTGGAGACCACTGCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTAAGGGGGAAGAAA 570
Db 924 CTGGACACCTTCTGTGCGAGTCCCTTATGCTGCCCCCAGAACTCTTCCAGGGCAAAAAA 983
QY 571 TATGATGGCCCGCGGACAGATGTCGAGCTGTGGAGTCACTCTTTCGCCCTGCTCGTG 630
Db 984 TATGATGGACCCGAGGTGGATGTGGAGCTAGGAGTTATCTCTATACACTGGTCAGC 1043
QY 631 GGGGCTCTGCCCTTTGATGACGACAACTCCGCCAGCTGTCGAGAAGGTGAACCGGGC 690
Db 1044 GATCCCTGCTTTGATGACGACAACTCAAGAGCTGCGGGAACCGGGTACTGAGGGGA 1103
QY 691 GTCTTCACATGCCCCATTCATTCCTCCAGATTGCCAGAGCTCTCTGAGGGAATGATC 750
Db 1104 AATACCGTATTCATTCCTACATGTCAGGACTGTGAAACCTGCTTAAGAAATTTCTC 1163
QY 751 GAAGTGGAGCCGGAAGAGCTCAGTCTGAGCAAAATTCAGAAACATCTCTGTTACCTA 810
Db 1164 ATTCTTAATCCCAAGAGAGGCACTTTAGAGCAATCATGAAGATCGATGATGAAT 1223
QY 811 G-----CGGGAAACACGAGCCAGACCCGTCGCTGGAGCCAGCCCTGCGCGCGGGTA 864
Db 1224 GTGGTCCAGAGATGATGAATTAAGCCTTACGTGGAGCACTCCCTGACTACAGGAC 1283
QY 865 GCCATGCGGA 874
Db 1284 CCGCGGCGGA 1293

RESULT 12
US-09-949-016-1547
; Sequence 1547, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1547
; LENGTH: 2950
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1547

Query Match 8.7%; Score 199.2; DB 4; Length 2950;
Best Local Similarity 59.2%; Pred. No. 2.6e-38;
Matches 361; Conservative 0; Mismatches 243; Indels 6; Gaps 1;
QY 271 TACCTGGTTCTGGAGACAGCTCTCGGGGGGTGAGCTATTTCGACTACTCGTAAAGAGGG 330
Db 684 TACCTGTGATGAGTACCTAGTGGCGGAGAGGATTTTGAATTAACCTAGTGGCTCATGGC 743
QY 331 AGACTGACGCCCAAGAGAGCCGAAAGTTCTTCGCCAGATGTGTCTGCGCTGGACTTC 390
Db 744 AGGATGAAGAAAGAGAGCTGAGCCAAATTCGCCAGATGATGTCTGCTGTCAGTAC 803
QY 391 TGCCACAGCTACTCCATCTGCCACAGACCTTAAGCCCGAGAACTTGCTTTTGGATGAG 450
Db 804 TGTCCACAGAGTTTATTGTGTCATAGAGACTTAAGGCGAGAAACCTGCTCTTGGATGCT 863
QY 451 AAAAAACAATCGGCAATTCAGACTTCGGCATGGCGTCCCTGCGAGGTGGGGGACAGCCTC 510

Db 864 GATATGAACATCAAGATTGCAGACTTTTGGCTTCAGCAATGAATTCACCTTTTGGGAACAAG 923
QY 511 CTGGAGACCACTGCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTAAGGGGGAAGAAA 570
Db 924 CTGGACACCTTCTGTGCGAGTCCCTTATGCTGCCCCCAGAACTCTTCCAGGGCAAAAAA 983
QY 571 TATGATGGCCCGCGGACAGATGTCGAGCTGTGGAGTCACTCTTTCGCCCTGCTCGTG 630
Db 984 TATGATGGACCCGAGGTGGATGTGGAGCTAGGAGTTATCTCTATACACTGGTCAGC 1043
QY 631 GGGGCTCTGCCCTTTGATGACGACAACTCCGCCAGCTGTCGAGAAGGTGAACCGGGC 690
Db 1044 GATCCCTGCTTTGATGACGACAACTCAAGAGCTGCGGGAACCGGGTACTGAGGGGA 1103
QY 691 GTCTTCACATGCCCCATTCATTCCTCCAGATTGCCAGAGCTCTCTGAGGGAATGATC 750
Db 1104 AATACCGTATTCATTCCTACATGTCAGGACTGTGAAACCTGCTTAAGAAATTTCTC 1163
QY 751 GAAGTGGAGCCGGAAGAGCTCAGTCTGAGCAAAATTCAGAAACATCTCTGTTACCTA 810
Db 1164 ATTCTTAATCCCAAGAGAGGCACTTTAGAGCAATCATGAAGATCGATGATGAAT 1223
QY 811 G-----CGGGAAACACGAGCCAGACCCGTCGCTGGAGCCAGCCCTGCGCGCGGGTA 864
Db 1224 GTGGTCCAGAGATGATGAATTAAGCCTTACGTGGAGCACTCCCTGACTACAGGAC 1283
QY 865 GCCATGCGGA 874
Db 1284 CCGCGGCGGA 1293

RESULT 13
US-09-984-890-1
; Sequence 1, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL001306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-890-1

Query Match 8.6%; Score 197.6; DB 4; Length 2175;
Best Local Similarity 59.0%; Pred. No. 5.7e-38;
Matches 360; Conservative 0; Mismatches 244; Indels 6; Gaps 1;
QY 271 TACCTGGTTCTGGAGACAGCTCTCGGGGGGTGAGCTATTTCGACTACTCGTAAAGAGGG 330
Db 376 TACCTTGTGATGAGTACGCTAGTGGCGGAGAGGATTTGATTAACCTAGTGGCTCATGGC 435
QY 331 AGACTGACGCCCAAGAGAGCCGAAAGTTCTTCGCCAGATGTGTCTGCGCTGGACTTC 390
Db 436 AGGATGAAGAAAGAGGCTCGAGCCAAATTCGCCAGGTAGTGTCTGCTGTGCAGTAC 495
QY 391 TGCCACAGCTACTCCATCTGCCACAGACCTTAAGCCCGAGAACCTGCTTTTGGATGAG 450
Db 496 TGTCCACAGAAAGTTTATTGTCTCATAGAGACTTAAGGCGAGAAACCTGCTCTTGGATGCT 555
QY 451 AAAAAACAATCCGCAATTCAGACTTCGGCATGGCGTCCCTGCGAGGTGGGGGACAGCCTC 510
Db 556 GATATGAACATCAAGATTGAGACTTTGGCTTCAGCAATGAATTCACCTTTTGGGAACAAG 615
QY 511 CTGGAGACCACTGCGGGTCCCGCATATGCGGTGTCAGAGGTGATTAAGGGGGGAAAAA 570

Db 616 CTGACACCTTCYGTGGAGTCCCTTATGCTGCCCGAGACTCTCCAGGGCAAAA 675
Qy 571 TATGATGCCCGCCGGGAGACATGTGAGCTGTGGAGTCAATCTCTTCGCGCTCTCGTG 630
Db 676 TATGATGGAACCGGAGGTGGATGTGTGAGCTAGGAGTTATCTCTATACACTGGTCAGC 735
Qy 631 GGGGCTCTGCGCTTTGATGACGACAACTCCCGCAGCTGTGGAGAGAGGTGAACGGGGC 690
Db 736 GGATCCCTGCGCTTTGATGAGCAGAACCTCAAGAGAGCTGGGGAACGGGTACTGAGGGGA 795
Qy 691 GTCTTCCACATGCCCGCCCACTTCATCTCCAGATTGCCAGAGCTCTCGAGGGGAATGATC 750
Db 796 AATACCGTATTCATTTCTATATGTCACGACTGTGAAACCTGCTTTAGAAATTTCTC 855
Qy 751 GAAGTGGAGCCGAAAAAGGCTCAGTCTGAGCAAAATTCAGAAACATCTCTTGGTACCTA 810
Db 856 ATTCTTAATCCAGCAAGAGAGGCACTTTAGAGCAAAATCATGAAGATCGATGATGAAT 915
Qy 811 G-----GCGGGAACAGAGCCAGACCGTGTGCTGAGCCAGCCCTTGGCGCGGGTA 864
Db 916 GTGGGTCAACGAAGATGATGAACCTTAAGGCTTTACGTGGAGCCACTCCCTGACTACAAGGAC 975
Qy 865 GCCATGCCGA 874
Db 976 CCCCGCGGA 985

RESULT 14

US-10-274-194-1
; Sequence 1, Application US/10274194
; Patent No. 6706511
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE REFERENCE: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306DIV
; CURRENT APPLICATION NUMBER: US/10/274,194
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-274-194-1

Query Match 8.6%; Score 197.6; DB 4; Length 2175;
Best Local Similarity 59.0%; Pred. No. 5.7e-38;
Matches 360; Conservative 0; Mismatches 244; Indels 6; Gaps 1;
Qy 271 TACCTGTCTCTGGAGCAGCTCTCGGGGGTGGAGCTATTCGACTACCTGGTAAAGAGGGG 330
Db 376 TACCTGTCTATGAGTAGCTAGTGTGGCGGAGAGTATTTGATACCTAGTGGCTCATGGC 435
Qy 331 AGACTGACGCCCAAGGAGGCCGAAAGTCTTCGCCAGATTTGTCTGCGCTGGACTTC 390
Db 436 AGGATGAAGAAAGAGGCTCGAGCCAAATTCGCCAGGTAGTGTCTGCTGTGCAGTAC 495
Qy 391 TGCACAGCTACTCCATCTGCGCAGACACTAAAGCCCGAGAACCTGTCTTTGGATGAG 450
Db 496 TGTCAACAGAGTTTATTTGTCATAGAGACTTAAAGGCAAGAAACCTGCTCTTGGATGCT 555
Qy 451 AAAAAACAATCCGATTTGAGACTTCGGCATGCGCTCCCTGCAAGTGGGGGAGCAGCTC 510
Db 556 GATATGAACATCAAGATTGAGACTTTGGCTTCAGCAATGAATTCACCTTTGGGAAACAAG 615
Qy 511 CTGAGACCAAGCTCGGGTCCCGCCATTATGCGTGTCCAGAGGTGATTAAAGGGGAAAAA 570
Db 616 CTGACACCTTCYGTGGAGTCCCTTATGCTGCCCGCAGACTCTCCAGGGCAAAA 675
Qy 571 TATGATGCCCGCGGCGAGACATGTGAGCTGTGAGTCAATCTCTTCCTCTTCGCGCTCTCGTG 630

Db 676 TATGATGGAACCGGAGGTGGATGTGTGAGCCTAGGAGTTATCTCTATACACTGGTCAGC 735
Qy 631 GGGGCTCTGCGCTTTGATGACGACAACTCCCGCAGCTGTGGAGAGAGGTGAACGGGGC 690
Db 736 GGATCCCTGCGCTTTGATGAGCAGAACCTCAAGAGAGCTGGGGAACGGGTACTGAGGGGA 795
Qy 691 GTCTTCCACATGCCCGCCCACTTCATCTCCAGATTGCCAGAGCTCTCGAGGGGAATGATC 750
Db 796 AATACCGTATTCATTTCTATATGTCACGACTGTGAAACCTGCTTTAGAAATTTCTC 855
Qy 751 GAAGTGGAGCCGAAAAAGGCTCAGTCTGAGCAAAATTCAGAAACATCTCTTGGTACCTA 810
Db 856 ATTCTTAATCCAGCAAGAGAGGCACTTTAGAGCAAAATCATGAAGATCGATGATGAAT 915
Qy 811 G-----GCGGGAACAGAGCCAGACCGTGTGCTGAGCCAGCCCTTGGCGCGGGTA 864
Db 916 GTGGGTCAACGAAGATGATGAACCTTAAGGCTTTACGTGGAGCCACTCCCTGACTACAAGGAC 975
Qy 865 GCCATGCCGA 874
Db 976 CCCCGCGGA 985

RESULT 15

US-08-557-006C-38
; Sequence 38, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajinder K.
; APPLICANT: Carling, David A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 38
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: Human AMP protein kinase
US-08-557-006C-38

Query Match 7.1%; Score 163; DB 3; Length 1742;
Best Local Similarity 56.7%; Pred. No. 1.3e-29;
Matches 301; Conservative 0; Mismatches 230; Indels 0; Gaps 0;
Qy 275 TGGTTCTGGAGCAGCTCTCGGGGGTGGAGCTATTCGACTACCTGGTAAAGAGGGGAGAC 334
Db 272 TGGTAATGGAATATGTCTCTGGAGGTGAATTTGTCGACTACATCTGTAAACACAGGGAGG 331
Qy 335 TGACGCCCAAGGAGGCCGAAAGTCTTCGCCAGATTTGTCTGCGCTGGACTTCTGCC 394
Db 332 TTGAAGAGGTGGAAGCTCGCGGCTCTTCAGCAGATTTCTGTCTGCCGTGGACTACTGTC 391
Qy 395 ACAGCTACTCCATCTGTCACAGAGACCTAAAGCCCGAGAACCTCTTTTGGATGAGAAAA 454
Db 392 ACAGGCACATGGTTGTGCCACAGGGACCTGAAGCCAGAGACGTTGCTGGACGCCCAGA 451
Qy 455 ACAACATCCGATTCAGACTTCGGCATGGCGTCCCTGCGAGGTGGGGGAGCAGCTCTCGG 514
Db 452 TGAATGCTAAGATAGCTGACTTCGGACTCTCTAATATGATGTTCAGATGGTGAATTTCTAC 511
Qy 515 AGACCACTCGGGTCCCGCCATTATGCGTGTCCAGAGGTGATTAAGGGGGGAAAAATATG 574
Db 512 GAACCTAGCTGTGATGCCCAAAATTAAGCAGACCGGAGGTCAATCTCAGGAAGGCTGATG 571

Tue Feb 22 14:35:29 2005

Qy	575	ATGCGCCCGGGCAGACATGTGAGCTGTGAGTCACTCTTCGCCCTGCTCGTGGGG	634
Db	572	CGGTCCTGAGGTTGATATCTGGAGCTGTGGTGTATCTCTGTATGCCCTTCTCTGTGGCA	631
Qy	635	CTCTGCCCTTTGATGACGACAACTCCGCCAGCTGTGGAGAGGTGAACGGGGCGTCT	694
Db	632	CCCTCCCGTTGACGATGACACGTGCTACGCTCTTTAAGAAGATCCGAGGGGTGTGT	691
Qy	695	TCCACATGCCCCACTTCATTCTCTCCAGATTGCCAGAGCCTCTTGAGGGGAATGATCGAAG	754
Db	692	TCTACATCCCGGAGTATCTCAACGGTTCTATTGCCACTCTGTGTGATGCACATGCTGCAGG	751
Qy	755	TGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCCTTGGT	805
Db	752	TGGACCCCTTGAGCGGAGCAACTATCAAGACATACGAGAGCATGAATGGT	802

Search completed: February 19, 2005, 14:27:39
Job time : 415 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - protein search, using sw model
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(without alignments)
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Perfect score: 4056
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003s:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4056	100.0	762	6	AB98744 Human kin
2	3545	87.4	703	6	AB98745 Human kin
3	3545	87.4	715	7	AD71299 Novel hum
4	3545	87.4	715	7	AD71417 Human nov
5	3545	87.4	778	6	AB98743 Human kin
6	3545	87.4	778	6	AAO23053 Human euk
7	3545	87.4	778	7	AD38431 Human pro
8	3545	87.4	778	8	ADL14128 Novel hum
9	3545	87.4	778	8	ADQ89184 Human uro
10	3545	87.4	778	8	ADL16426 Human euk
11	3545	87.4	794	4	AAU03517 Human pro
12	3545	87.4	794	5	AAE16271 Human kin
13	3362	82.9	754	6	AAO16604 Human cel
14	2467	60.8	473	8	ADQ65624 Novel hum
15	2400	59.2	766	8	ADR50797 Human c-b
16	2390.5	58.9	585	6	ABG72383 Human ser
17	2390.5	58.9	585	7	ABW00449 Human ser
18	2390.5	58.9	585	8	ADH59078 Human KSE
19	2387.5	58.9	674	6	AAO29858 Human kin
20	2387.5	58.9	674	8	ADJ96621 Human cal
21	2386.5	58.8	608	5	ABO09558 Human kin
22	2386.5	58.8	664	5	AAE21723 Human PKI
23	2386.5	58.8	668	5	ABO09557 Human kin
24	2386.5	58.8	668	6	ABG72382 Human ser
25	2386.5	58.8	668	7	ABW00448 Human ser

26	2386.5	58.8	668	8	ADH59076	Adh59076 Human KSE
27	2381.5	58.7	603	8	ADH59091	Adh59091 Human KSE
28	2381.5	58.7	674	5	AAm47830	AAm47830 Human pro
29	2381.5	58.7	674	6	ABR44014	ABr44014 Human ser
30	2366.5	58.3	636	6	AAO29859	AAo29859 Human kin
31	1590	39.2	851	4	ABG62061	ABb62061 Drosophil
32	1043	25.7	204	4	ABBI1680	ABb11680 Human Ser
33	979	24.1	301	4	ABBI1052	ABb11052 Human Hrp
34	677	16.7	1518	6	ABR53219	ABr53219 Protein s
35	677	16.7	1518	7	ADK63724	ADk63724 Disease t
36	677	16.7	1518	8	ADI26784	ADI26784 Saccharom
37	677	16.7	1518	8	ADS43813	ADs43813 Bacterial
38	657	16.2	1462	8	ADI26788	ADI26788 Candida a
39	651	16.1	1349	4	AAO70854	AAg70854 C albican
40	648	16.0	1251	4	AAAB5626	AAb5626 Novel pro
41	648	16.0	1309	7	ADG74678	ADg74678 Human kin
42	648	16.0	1311	8	ADI29232	ADI29232 Human MAR
43	648	16.0	1349	8	ADI26789	ADI26789 Candida a
44	648	16.0	1369	5	AAE21712	AAe21712 Human PKI
45	643.5	15.9	783	4	AAAG65764	AAg65764 Human pro

ALIGNMENTS

RESULT 1
ABB98744
ID ABB98744 standard; protein; 762 AA.
XX ABB98744;
XX AC
XX AD
DT 20-JAN-2003 (first entry)
XX
DE Human kinase #2.
XX
KW Human; kinase; chromosome 19.
XX
OS Homo sapiens.
XX
PN WO200281670-A1.
XX
PD 17-OCT-2002.
XX
PF 04-APR-2002; 2002WO-US010786.
XX
PR 06-APR-2001; 2001US-0282036P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
XX Turner CA, Mathur B, Friddle CJ;
XX WPI; 2003-058538/05.
XX N-PSDB; ABV74558.
XX
XX New human kinase proteins useful for diagnosis, drug screening, clinical
XX trial monitoring, treatment of disorders and diseases, and cosmetic and
XX nutritional applications.
XX
XX Claim 5; Page 42-43; 47pp; English.
XX
XX The present sequence is a novel human kinase. The genomic locus encoding
XX the kinase is thought to be on human chromosome 19. The kinase and its
XX coding sequence are useful for diagnosis, drug screening, clinical trial
XX monitoring, treatment of disorders and diseases, and cosmetic and
XX nutritional applications
XX
XX Sequence 762 AA;

Query Match 100.0%; Score 4056; DB 6; Length 762;
Best Local Similarity 100.0%; Pred. No. 4.9e-270;
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MGLEFGFLEAGNWSHFLPGSDGNWNLFLPGINGNWSLFLPGTHGNWSLFLPRIMGIVL 60

Db 1 MGLEFGLEAGGNWHLFGSDGNWNLFLPGINGNWSLFLPGTHGNSLFLPRIMGIVL 60
Qy 61 CHQEPVEVGEALWSCTCFPPSAPSISFRYLVLHVSGGELFDYLVKKGRLTPKEARKE 120
Db 61 CHQEPVEVGEALWSCTCFPPSAPSISFRYLVLHVSGGELFDYLVKKGRLTPKEARKE 120
Qy 121 FROIVSALDFCHSYISICHRDLKPENLLDEKNNIRIADFGMASLQVGDLSLETSCGSPHY 180
Db 121 FROIVSALDFCHSYISICHRDLKPENLLDEKNNIRIADFGMASLQVGDLSLETSCGSPHY 180
Qy 181 ACEPVKGEKYDGRADMWSCGVILFALLVGVLPDDNLRQLLEKVKRGVFMHPHFIPP 240
Db 181 ACEPVKGEKYDGRADMWSCGVILFALLVGVLPDDNLRQLLEKVKRGVFMHPHFIPP 240
Qy 241 DCQSLRGMIEVEPEKRLSLEQIKHPWYLGKHEDPCLEPAPGRVAMRSIPLSNGELD 300
Db 241 DCQSLRGMIEVEPEKRLSLEQIKHPWYLGKHEDPCLEPAPGRVAMRSIPLSNGELD 300
Qy 301 PDVLESWASLGCFRDRERLHRELSEENQEKMIYVLLDRKERYPSCEDQDLPPRNDVD 360
Db 301 PDVLESWASLGCFRDRERLHRELSEENQEKMIYVLLDRKERYPSCEDQDLPPRNDVD 360
Qy 361 PPRKRVDSPLSRHGKRRPERKSNVLSITDAGGGSPVPTRRALEMAQHSQRSVSAGA 420
Db 361 PPRKRVDSPLSRHGKRRPERKSNVLSITDAGGGSPVPTRRALEMAQHSQRSVSAGA 420
Qy 421 STGLSSPLSPSPSPVPSFPEPCAGDEARGGSPSTOTLPSRGRGGGAGEQPPPPS 480
Db 421 STGLSSPLSPSPSPVPSFPEPCAGDEARGGSPSTOTLPSRGRGGGAGEQPPPPS 480
Qy 481 ARSTPLPGPCSPRSSSGTPLHSLHTPRASPTGTCTTTPPPSPGGVGGAAWRSRLNSI 540
Db 481 ARSTPLPGPCSPRSSSGTPLHSLHTPRASPTGTCTTTPPPSPGGVGGAAWRSRLNSI 540
Qy 541 RNSFLGSPFRHRRKQVPTAEEMSLTPESPPELAKRSWFCNFIISLDKEQIFLVLDKXP 600
Db 541 RNSFLGSPFRHRRKQVPTAEEMSLTPESPPELAKRSWFCNFIISLDKEQIFLVLDKXP 600
Qy 601 LSSIKADIVHAFLSIPLSHSVLSQTSFRAEYKASGSPVFKVRFQVDIISSEGEPS 660
Db 601 LSSIKADIVHAFLSIPLSHSVLSQTSFRAEYKASGSPVFKVRFQVDIISSEGEPS 660
Qy 661 PRDGGSGGGIYSVFTLISGFSRRFRVETIQALLSTHDQPSVQALADEKNGAOTRP 720
Db 661 PRDGGSGGGIYSVFTLISGFSRRFRVETIQALLSTHDQPSVQALADEKNGAOTRP 720
Qy 721 AGAPPRSLQPPGPRDPELSSSPRGGPKKLLATNGTPLP 762
Db 721 AGAPPRSLQPPGPRDPELSSSPRGGPKKLLATNGTPLP 762

RESULT 2
ABB98745
ID ABB98745 standard; protein; 703 AA.

XX AC ABB98745;
XX DT 20-JAN-2003 (first entry)
XX DE Human kinase #3.
XX KW Human; kinase; chromosome 19.
XX OS Homo sapiens.
XX FN WO200281670-A1.
XX PD 17-OCT-2002.
XX PF 04-APR-2002; 2002WO-US010786.
XX PR 06-APR-2001; 2001US-0282036P.

XX (LEXI-) LEXICON GENETICS INC.
PA Turner CA, Mathur B, Friddle CJ;
XX WPI; 2003-058538/05.
XX N-PSDB; ABV74559.
XX New human kinase proteins useful for diagnosis, drug screening, clinical
PT trial monitoring, treatment of disorders and diseases, and cosmetic and
PT nutritional applications.
XX Claim 5; Page 44-46; 47pp; English.
XX The present sequence is a novel human kinase. The genomic locus encoding
CC the kinase is thought to be on human chromosome 19. The kinase and its
CC coding sequence are useful for diagnosis, drug screening, clinical trial
CC monitoring, treatment of disorders and diseases, and cosmetic and
CC nutritional applications
XX Sequence 703 AA;
SQ Query Match 87.4%; Score 3545; DB 6; Length 703;
Best Local Similarity 99.7%; Pred. No. 6.1e-235;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 89 FRYLVLEHVSGGELFDYLVKKGRLTPKEARKEFRQIVSALDFCHSYISICHRDLKPENLL 148
Db :
30 YLYLVLEHVSGGELFDYLVKKGRLTPKEARKEFRQIVSALDFCHSYISICHRDLKPENLL 89
Qy 149 DEKNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVKEKYDGRADMWSCGVILFAL 208
Db 90 DEKNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVKEKYDGRADMWSCGVILFAL 149
Qy 209 LVGALPFDNLRQLLEKVKRGVFMHPHFIPDCQSLRGMIEVEPEKRLSLEQIKHPW 268
Db 150 LVGALPFDNLRQLLEKVKRGVFMHPHFIPDCQSLRGMIEVEPEKRLSLEQIKHPW 209
Qy 269 YLGKHEPDPCLPAPGRVAMRSIPLSNGELDPDVLESWASLGCFRDRERLHRELSEEE 328
Db 210 YLGKHEPDPCLPAPGRVAMRSIPLSNGELDPDVLESWASLGCFRDRERLHRELSEEE 269
Qy 329 NQSKMIYVLLDRKERYPSCEDQDLPPRNDVDPPRKRVDSPMLSRHGKRRPERKSNVLS 388
Db 270 NQSKMIYVLLDRKERYPSCEDQDLPPRNDVDPPRKRVDSPMLSRHGKRRPERKSNVLS 329
Qy 389 ITDAGGGSPVPTRRALEMAQHSQRSVSAGSTGLSSPLSPSPVPSFPEPCAGDE 448
Db 330 ITDAGGGSPVPTRRALEMAQHSQRSVSAGSTGLSSPLSPSPVPSFPEPCAGDE 389
Qy 449 ARGGSPTSKTQTLPSRGRGGGAGEQPPPPSARSTPLPGPCSPRSSSGTPLHSLHTP 508
Db 390 ARGGSPTSKTQTLPSRGRGGGAGEQPPPPSARSTPLPGPCSPRSSSGTPLHSLHTP 449
Qy 509 RASPTGTGTTPPPSPGGVGGAAWRSRLNSIRNSFLGSPFRHRRKQVPTAEEMSLTP 568
Db 450 RASPTGTGTTPPPSPGGVGGAAWRSRLNSIRNSFLGSPFRHRRKQVPTAEEMSLTP 509
Qy 569 ESSPELAKRSWFCNFIISLDKEQIFLVLDKDKPLSSIKADIVHAFLSIPLSHSVLSQTSF 628
Db 510 ESSPELAKRSWFCNFIISLDKEQIFLVLDKDKPLSSIKADIVHAFLSIPLSHSVLSQTSF 569
Qy 629 RAEYKASGSPVFKVRFQVDIISSEGEPSPRDGGSGGGIYSVFTLISGFSRRFRK 688
Db 570 RAEYKASGSPVFKVRFQVDIISSEGEPSPRDGGSGGGIYSVFTLISGFSRRFRK 629
Qy 689 VVETIQALLSTHDQPSVQALADEKNGAOTRPAGAPPRSLQPPGPRDPELSSSPRGGPP 748
Db 630 VVETIQALLSTHDQPSVQALADEKNGAOTRPAGAPPRSLQPPGPRDPELSSSPRGGPP 689
Qy 749 KDKKLLATNGTPLP 762
Db 690 KDKKLLATNGTPLP 703

RESULT 3

AD71299 standard; protein; 715 AA.

AC ADE71299;

DT 29-JAN-2004 (first entry)

XX Novel human protein #53.

DE human; novel protein; drug.

XX Homo sapiens.

XX JP2002345493-A.

PD 03-DEC-2002.

XX 29-MAR-2001; 2002JP-00049046.

XX 29-MAR-2001; 2001JP-00095524.

PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.

XX WPI; 2003-460885/44.

DR N-PSDB; ADE71237.

XX A gene and a protein encoded by it, used in drugs.

PS Disclosure; Page 227-230; 257pp; Japanese.

XX The invention comprises the amino acid and coding sequences of novel human proteins. The DNA and protein sequences of the invention are used in drugs. The present amino acid sequence represents a novel human protein of the invention.

XX Sequence 715 AA;

Query Match 87.4%; Score 3545; DB 7; Length 715;
Best Local Similarity 99.7%; Pred. No. 6.2e-235;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 89 FRYLVLEHVGGEFLDYLVKGRITPKKARFFQIVSALDFCHSYICHRLDKPENLL 148
DB 42 YLYLVLEHVGGEFLDYLVKGRITPKKARFFQIVSALDFCHSYICHRLDKPENLL 101
QY 149 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADMWSCGVILPAL 208
DB 102 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADMWSCGVILPAL 161
QY 209 LVGALPFDDNNLRLLEKVKGVFHMHPHFIIPDCQSLRLGMIEVEPEKRLSLEQIQKHPW 268
DB 162 LVGALPFDDNNLRLLEKVKGVFHMHPHFIIPDCQSLRLGMIEVEPEKRLSLEQIQKHPW 221
QY 269 YLGKHEPDPCLPAPGRVAMRSLPSNGELDPDVLSEMASLGCFRDRERLHRELSEEE 328
DB 222 YLGKHEPDPCLPAPGRVAMRSLPSNGELDPDVLSEMASLGCFRDRERLHRELSEEE 281
QY 329 NOEKMIYLLDRKERYPCEDQDLPDRNDVDPKRVDSFPMLSHGKRRPERKSMVLS 389
DB 282 NOEKMIYLLDRKERYPCEDQDLPDRNDVDPKRVDSFPMLSHGKRRPERKSMVLS 341
QY 389 ITDAGGGSVPVTRALEMAHORSRSVSGASTGLSSPLSSPRSPVSPSPGAGDE 448
DB 342 ITDAGGGSVPVTRALEMAHORSRSVSGASTGLSSPLSSPRSPVSPSPGAGDE 401
QY 449 ARGGGSPTKTQTLPSPRGCGGAGEQPPPSARSTPLPGPGSPRSGGTPLHSPHLP 508
DB 402 ARGGGSPTKTQTLPSPRGCGGAGEQPPPSARSTPLPGPGSPRSGGTPLHSPHLP 461
QY 509 RASPTGTGTTTPPPSGGCGAAWRSLNIRNSFLGSPRFRHRKMQVPTAEEMSSLTP 568

Db 462 RASPTGTGTTTPPPSGGCGAAWRSLNIRNSFLGSPRFRHRKMQVPTAEEMSSLTP 521
QY 569 ESSPELAKRSWFGNFISLDKEEQIFLVLDKDKPLSSIKADIVHAFPLSPSLSHSVLSQTSF 628
Db 522 ESSPELAKRSWFGNFISLDKEEQIFLVLDKDKPLSSIKADIVHAFPLSPSLSHSVLSQTSF 581
QY 629 RAEYKASGSPSVQKPVRFQVDISSSEGEPEPSRRDGGGGGIIYVTFLLISGSRPRPKR 688
Db 582 RAEYKASGSPSVQKPVRFQVDISSSEGEPEPSRRDGGGGGIIYVTFLLISGSRPRPKR 641
QY 689 VVETIOAQLLSTHDQPSVQALADEKGAQTRPAGAPRSLQPPGPRDPPELSSSPRGGPP 748
Db 642 VVETIOAQLLSTHDQPSVQALADEKGAQTRPAGAPRSLQPPGPRDPPELSSSPRGGPP 701
QY 749 KDKKLLATNGTPLP 762
Db 702 KDKKLLATNGTPLP 715

RESULT 4

ADF74177

ID ADF74177 standard; protein; 715 AA.

XX AC ADF74177;

DT 26-FEB-2004 (first entry)

XX Human novel brain/hippocampus protein #65.

XX Human; brain; hippocampus; gene therapy; mental illness;
XX proteome analysis.

XX Homo sapiens.

XX JP2003009886-A.

XX 14-JAN-2003.

XX 21-DEC-2001; 2001JP-00390441.

XX 22-DEC-2000; 2000JP-00389742.

XX 29-MAR-2001; 2001JP-00095524.

XX 25-APR-2001; 2001JP-00127066.

XX (KAZU-) ZH KAZUSA DNA KENKYUSHO.

XX (PROT-) PROTEIN EXPRESS KK.

XX WPI; 2003-735084/70.

XX N-PSDB; ADF74247.

XX Novel isolated polypeptide useful for screening compounds which modulate the activity of polypeptide and thus have therapeutic applications.

XX Claim 1; SEQ ID NO 65; 319pp; Japanese.

XX The invention relates to an isolated human polypeptide consisting of a sequence of any one of 70 fully defined sequences (S1) appearing as ADF74113-ADF74182 being encoded by one of 70 disclosed cDNA sequences isolated from brain or hippocampus tissue, or a sequence of (S1) having deletion, substitution, or addition and essentially retaining the same biological activity of (S1). Also included are DNA that encodes the protein, DNA which hybridizes with the encoding DNA and codes a polypeptide which substantially as the same activity as that of a polypeptide above, a gene including the DNA, a recombinant polypeptide encoded by the gene, an antibody against the protein, DNA chip which comprises the DNA, a polypeptide chip comprising the protein, an antibody chip comprising the antibody, a recombinant vector containing the DNA, a transformed host cell containing the vector, an antisense polynucleotide which has a sequence complementary to the DNA, a kit for screening compounds that interact with the protein, test compounds which interact with the protein and homologous proteins having 70% sequence identity with (S1). The protein is useful for identifying compounds which interact

CC with the protein e.g., compounds which inhibit or activate the protein.
CC Compounds that inhibit the protein activity are useful as therapeutic
CC agents for treating disorders characterised by aberrant protein activity.
CC The DNA is useful for producing the protein by recombinant techniques, as
CC a probe in diagnostic techniques for detecting abnormalities in the gene,
CC and in gene therapy techniques. The DNA is useful for creating animal
CC models of disease. The DNA chips are useful for diagnosing any
CC abnormalities of the DNA in biological samples obtained from human
CC subjects, where the abnormalities result in mental illness. The antibody
CC chip is useful for detecting the protein in biological samples. The protein
CC chip is useful for functional analysis of the protein, e.g. expression of
CC the protein, interaction of the protein, post-translational modification
CC of the protein. The antibody chip is useful for analysing disease states
CC associated with polypeptide. The antibody chip is also useful in proteome
CC analysis. The present sequence represents a human brain/hippocampus
CC protein of the invention.

XX SQ Sequence 715 AA;

Query Match 87.4%; Score 3545; DB 7; Length 715;
Best Local Similarity 99.7%; Pred. No. 6.2e-235;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 89 FRYLVLEHVGSGELFDYLVKKGLTPEAKRFFQIVSALDFCHSYISICHRDLKPNLL 148
DB 42 YLYLVLEHVGSGELFDYLVKKGLTPEAKRFFQIVSALDFCHSYISICHRDLKPNLL 101
QY 149 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIGKEVDGRRADWMSGVILFAL 208
DB 102 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIGKEVDGRRADWMSGVILFAL 161
QY 209 LVGALPDDNNLRQLLEKVKRGVFMHFFIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 268
DB 162 LVGALPDDNNLRQLLEKVKRGVFMHFFIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 221
QY 269 YLGKHEPDPCLPAPGRVAMRSLPSNGELDPVLESMAISLGCFRDRRLHRELSEEE 328
DB 222 YLGKHEPDPCLPAPGRVAMRSLPSNGELDPVLESMAISLGCFRDRRLHRELSEEE 281
QY 329 NOEKMIYLLLDKREYPCSDQDLPDNDVDPKRVDSPLSRHGKRRPERKSMVLS 388
DB 282 NOEKMIYLLLDKREYPCSDQDLPDNDVDPKRVDSPLSRHGKRRPERKSMVLS 341
QY 389 ITDAGGSGSPVPTTRALEMAHQSRSVSGASTGLSSPLSSPRSPVFSPPGAGDE 448
DB 342 ITDAGGSGSPVPTTRALEMAHQSRSVSGASTGLSSPLSSPRSPVFSPPGAGDE 401
QY 449 ARGGSGSPSTKTOTLPSRGRGGAGEQPPPSARSTPLPGPGRSSGGTPLHSPHTP 508
DB 402 ARGGSGSPSTKTOTLPSRGRGGAGEQPPPSARSTPLPGPGRSSGGTPLHSPHTP 461
QY 509 RASPTGTPTTTPPPGGVGGAAWRSLNSTRNSFLGSPRFRHRRKMVPTAEWSSILTP 568
DB 462 RASPTGTPTTTPPPGGVGGAAWRSLNSTRNSFLGSPRFRHRRKMVPTAEWSSILTP 521
QY 569 ESSPELAKESWFGNFISLDKEQIFVLVKDKPLSSIKADIVHAFISLPSLSHVSLSQTSF 628
DB 522 ESSPELAKESWFGNFISLDKEQIFVLVKDKPLSSIKADIVHAFISLPSLSHVSLSQTSF 581
QY 629 RAEYKASGSPVFOKRVQVDIISSEGEPPSPRDGGGGIYSVTTLISGSPRRFR 688
DB 582 RAEYKASGSPVFOKRVQVDIISSEGEPPSPRDGGGGIYSVTTLISGSPRRFR 641
QY 689 VVETIOALLSHDQPSVALADEKNAGQTRPAGAPRPSLQPPGKRPDELSSSPRGPP 748
DB 642 VVETIOALLSHDQPSVALADEKNAGQTRPAGAPRPSLQPPGKRPDELSSSPRGPP 701
QY 749 KDKKLLATNGTLP 762
DB 702 KDKKLLATNGTLP 715

ABB98743
ID ABB98743 standard; protein; 778 AA.

XX ABB98743;

XX 20-JAN-2003 (first entry)

XX Human kinase #1.

XX Human; kinase; chromosome 19.

XX Homo sapiens.

XX WO200281670-A1.

XX 17-OCT-2002.

XX 04-APR-2002; 2002WO-US010786.

XX 06-APR-2001; 2001US-0282036P.

XX (LEXI-) LEXICON GENETICS INC.

XX Turner CA, Mathur B, Friddle CJ;

XX WPI; 2003-058538/05.

XX N-PSDB; ABV74557.

XX New human kinase proteins useful for diagnosis, drug screening, clinical
XX trial monitoring, treatment of disorders and diseases, and cosmetic and
XX nutritional applications.

XX Claim 5; Page 40-41; 47pp; English.

XX The present sequence is a novel human kinase. The genomic locus encoding
XX the kinase is thought to be on human chromosome 19. The kinase and its
XX coding sequence are useful for diagnosis, drug screening, clinical trial
XX monitoring, treatment of disorders and diseases, and cosmetic and
XX nutritional applications

XX SQ Sequence 778 AA;

Query Match 87.4%; Score 3545; DB 6; Length 778;
Best Local Similarity 99.7%; Pred. No. 6.9e-235;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 89 FRYLVLEHVGSGELFDYLVKKGLTPEAKRFFQIVSALDFCHSYISICHRDLKPNLL 148
DB 105 YLYLVLEHVGSGELFDYLVKKGLTPEAKRFFQIVSALDFCHSYISICHRDLKPNLL 164
QY 149 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIGKEVDGRRADWMSGVILFAL 208
DB 165 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIGKEVDGRRADWMSGVILFAL 224
QY 209 LVGALPDDNNLRQLLEKVKRGVFMHFFIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 268
DB 225 LVGALPDDNNLRQLLEKVKRGVFMHFFIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 284
QY 269 YLGKHEPDPCLPAPGRVAMRSLPSNGELDPVLESMAISLGCFRDRRLHRELSEEE 328
DB 285 YLGKHEPDPCLPAPGRVAMRSLPSNGELDPVLESMAISLGCFRDRRLHRELSEEE 344
QY 329 NOEKMIYLLLDKREYPCSDQDLPDNDVDPKRVDSPLSRHGKRRPERKSMVLS 388
DB 345 NOEKMIYLLLDKREYPCSDQDLPDNDVDPKRVDSPLSRHGKRRPERKSMVLS 404
QY 389 ITDAGGSGSPVPTTRALEMAHQSRSVSGASTGLSSPLSSPRSPVFSPPGAGDE 448
DB 405 ITDAGGSGSPVPTTRALEMAHQSRSVSGASTGLSSPLSSPRSPVFSPPGAGDE 464
QY 449 ARGGSGSPSTKTOTLPSRGRGGAGEQPPPSARSTPLPGPGRSSGGTPLHSPHTP 508
DB 465 ARGGSGSPSTKTOTLPSRGRGGAGEQPPPSARSTPLPGPGRSSGGTPLHSPHTP 524

Qy 509 RASPTGPTGTTTPSPGCGVGAARSLNSIRNSFLGSPRFRHRRKQVPTAEEMSLTP 569
 Db 525 RASPTGPTGTTTPSPGCGVGAARSLNSIRNSFLGSPRFRHRRKQVPTAEEMSLTP 584
 Qy 569 ESSPELAKRSWFGNFISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628
 Db 585 ESSPELAKRSWFGNFISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644
 Qy 629 RAEYKASGGPSVFOKPVRFQVDISSSEGPSPRRDGSQGGGIYSVFTTLLSGPSRRPKR 688
 Db 645 RAEYKASGGPSVFOKPVRFQVDISSSEGPSPRRDGSQGGGIYSVFTTLLSGPSRRPKR 704
 Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPRDPPELSSSPRRGPP 748
 Db 705 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPRDPPELSSSPRRGPP 764
 Qy 749 KDKKLLATNGTPLP 762
 Db 765 KDKKLLATNGTPLP 778

RESULT 6
 AA023053
 ID ARO23053 standard; protein; 778 AA.
 AC
 AC AAO23053;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Human eukaryotic protein kinase 55053 protein.
 XX
 KW Cardiant; antianginal; antiarteriosclerotic; antidiabetic; thyromimetic;
 KW antiarrhythmic; cytostatic; nootropic; neuroprotective; antiparkinsonian;
 KW anticonvulsant; antidepressant; tranquiliser; antimigraine; EPK 55053;
 KW eukaryotic protein kinase; cellular growth disorder; angina; cancer;
 KW cognitive; neurodegenerative; Alzheimer's disease; learning; hormone;
 KW autonomic function; memory; neuropsychiatric; depression; reproductive;
 KW musculoskeletal; immune system; human; enzyme.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 214..231
 FT /label= Transmembrane_domain
 XX
 PN WO2003042371-A2.
 XX
 PD 22-MAY-2003.
 XX
 PF 15-NOV-2002; 2002WO-US036967.
 XX
 PR 15-NOV-2001; 2001US-00003690.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Curtis RAJ;
 XX
 WPI: 2003-449574/42.
 XX
 N-PSDB; AAL55772.
 XX
 New isolated EPK-55053 nucleic acid and polypeptide, useful for
 diagnosing and treating EPK-55053-related disorders, such as
 hypertension, arteriosclerosis, myocardial infarction, diabetes mellitus,
 cancer and/or epilepsy.
 XX
 Claim 12; Fig 1A-1B; 86pp; English.
 PS
 XX The invention relates to a novel isolated nucleic acid molecule
 comprising a sequence which encodes a eukaryotic protein kinase (EPK) -
 55053 polypeptide. The polynucleotides and polypeptides of the invention
 may play a role as modulating agents in regulating a variety of cellular
 processes. Furthermore, the methods and compositions of the present

CC invention may be useful during the diagnosis, screening and treatment of
 CC various disorders including cellular growth-related disorders such as
 CC angina and cancer, cognitive and neurodegenerative disorders e.g.
 CC Alzheimer's disease, autonomic function disorders, learning or memory
 CC disorders and neuropsychiatric disorders such as depression. In addition,
 CC disorders associated with the musculoskeletal, reproductive and immune
 CC systems, as well as disorders which are cardiac or hormone related, may
 CC be addressed by the present invention. The current sequence is that of
 CC the human EPK-55053 protein of the invention
 XX
 SQ Sequence 778 AA;

Query Match 87.4%; Score 3545; DB 6; Length 778;
 Best Local Similarity 99.7%; Pred. No. 6.9e-235;
 Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 89 FRYLVLESHVSGGELFDYLVKKGRITPKAEKFFRQIVSALDFCHSYISICHRLDLPENLLL 148
 Db : |||||
 Qy 105 YLYLVLESHVSGGELFDYLVKKGRITPKAEKFFRQIVSALDFCHSYISICHRLDLPENLLL 164
 Db : |||||
 Qy 149 DEKNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIKGEKYGRRADMMSCGVILPAL 208
 Db : |||||
 Qy 165 DEKNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIKGEKYGRRADMMSCGVILPAL 224
 Db : |||||
 Qy 209 LVGALPEDDDNLRQLLEKVRGVFHPHFIPDCQSLRGMIIEVEPEKRLSLEQIQHPW 268
 Db : |||||
 Qy 225 LVGALPEDDDNLRQLLEKVRGVFHPHFIPDCQSLRGMIIEVEPEKRLSLEQIQHPW 284
 Db : |||||
 Qy 269 YLGKKEPDPCLPEAPGRVRVAMRSLPSNGELDPVLESMAISLGCFRDRERLHRLRSSEE 328
 Db : |||||
 Qy 285 YLGKKEPDPCLPEAPGRVRVAMRSLPSNGELDPVLESMAISLGCFRDRERLHRLRSSEE 344
 Db : |||||
 Qy 329 NQEKMIYLLLDKERYSPCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRERKSMVLS 388
 Db 345 NQEKMIYLLLDKERYSPCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRERKSMVLS 404
 Qy 389 ITDAGGGSVPVTRALEMAQHSQRSVSGASTGLSSPLSSPSRSPVFSFSPRGAGDE 448
 Db 405 ITDAGGGSVPVTRALEMAQHSQRSVSGASTGLSSPLSSPSRSPVFSFSPRGAGDE 464
 Qy 449 ARGGSPTSQTOTLPSRPGGGAGEQPPPSARSTPLPGPPSPRSGGTPLSPLHTP 508
 Db 465 ARGGSPTSQTOTLPSRPGGGAGEQPPPSARSTPLPGPPSPRSGGTPLSPLHTP 524
 Qy 509 RASPTGPTGTTTPSPGCGVGAARSLNSIRNSFLGSPRFRHRRKQVPTAEEMSLTP 568
 Db 525 RASPTGPTGTTTPSPGCGVGAARSLNSIRNSFLGSPRFRHRRKQVPTAEEMSLTP 584
 Qy 569 ESSPELAKRSWFGNFISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628
 Db 585 ESSPELAKRSWFGNFISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644
 Qy 629 RAEYKASGGPSVFOKPVRFQVDISSSEGPSPRRDGSQGGGIYSVFTTLLSGPSRRPKR 688
 Db 645 RAEYKASGGPSVFOKPVRFQVDISSSEGPSPRRDGSQGGGIYSVFTTLLSGPSRRPKR 704
 Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPRDPPELSSSPRRGPP 748
 Db 705 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPRDPPELSSSPRRGPP 764
 Qy 749 KDKKLLATNGTPLP 762
 Db 765 KDKKLLATNGTPLP 778

RESULT 7
 ADE38431
 ID ADE38431 standard; protein; 778 AA.
 AC
 AC ADE38431;
 XX
 DT 29-JAN-2004 (first entry)
 XX

KW human.
 XX Homo sapiens.
 OS US2004058355-A1.
 PN 25-MAR-2004.
 XX 25-APR-2003; 2003US-00423343.
 XX 30-SEP-1998; 98US-00163821.
 PR 27-JAN-1999; 99US-0117580P.
 PR 25-MAR-1999; 99US-00276400.
 PR 30-JUL-1999; 99US-00365162.
 PR 09-SEP-1999; 99US-00392189.
 PR 05-OCT-1999; 99US-00412210.
 PR 23-NOV-1999; 99US-00448076.
 PR 29-FEB-2000; 2000US-0186061P.
 PR 28-APR-2000; 2000US-0200688P.
 PR 19-MAY-2000; 2000US-0205447P.
 PR 30-JUN-2000; 2000US-00608921.
 PR 31-JUL-2000; 2000US-0221925P.
 PR 25-SEP-2000; 2000US-0234922P.
 PR 25-SEP-2000; 2000US-0235035P.
 PR 08-NOV-2000; 2000US-0246669P.
 PR 09-NOV-2000; 2000US-00711216.
 PR 14-NOV-2000; 2000US-0248325P.
 PR 15-NOV-2000; 2000US-0248893P.
 PR 22-DEC-2000; 2000US-0257511P.
 PR 05-JAN-2001; 2001US-0260166P.
 PR 28-FEB-2001; 2001US-00797039.
 PR 27-APR-2001; 2001US-00845044.
 PR 20-JUL-2001; 2001US-00909743.
 PR 31-JUL-2001; 2001US-00920346.
 PR 13-AUG-2001; 2001US-00928531.
 PR 14-AUG-2001; 2001US-00929218.
 PR 15-AUG-2001; 2001US-0312539P.
 PR 25-SEP-2001; 2001US-00963159.
 PR 08-NOV-2001; 2001US-00080016.
 PR 13-NOV-2001; 2001US-00012055.
 PR 15-NOV-2001; 2001US-00003690.
 PR 30-JAN-2002; 2002US-00060763.
 PR 25-MAR-2002; 2002US-00105989.
 PR 12-APR-2002; 2002US-00121911.
 PR 12-AUG-2002; 2002US-00217168.
 PR 22-OCT-2002; 2002US-00278036.
 PR 02-JAN-2003; 2003US-00336489.
 PR 03-JAN-2003; 2003US-00336153.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Kapeller-Libermann R, Hunter JJ, Meyers RE, Rudolph-Owen LA,
 PI Curtis RAJ, Olandt PJ, Tsai F, Galvin KM, Chun M, Williamson MJ;
 PI Silos-Santiago I, Bandaru R;
 XX WPI; 2004-268788/25.
 DR N-PSDB; ADL14127, ADL14129.
 XX New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529,
 PT 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593
 PT nucleic acid molecules and proteins, useful for treating, e.g. cancer,
 PT heart failure and angina.
 XX Claim 4; SEQ ID NO 11; 139pp; English.
 PS The invention describes an isolated 21910, 56634, 55053, 2504, 15977,
 CC 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217,
 CC 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising
 CC any one of 40 nucleotide sequences (I). The nucleic acid molecules and
 CC polypeptides are useful for diagnosing and treating a subject having a
 CC disorder, or a subject at risk of developing a disorder, which is
 CC associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501,
 CC 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983,

CC m1983, 38555 or 593 activity, such as cellular proliferative and/or
 CC differentiative disorders, brain disorders, platelet disorders, breast
 CC disorders, colon disorders, kidney (renal) disorders, lung disorders,
 CC ovarian disorders, prostate disorders, cervical disorders, spleen
 CC disorders, thymus disorders, thyroid disorders, testes disorders,
 CC hematopoietic disorders, pancreatic disorders, skeletal muscle disorders,
 CC skin (dermal) disorders, disorders associated with bone metabolism,
 CC immune, e.g. inflammatory disorders, cardiovascular disorders,
 CC endothelial cell disorders, liver disorders, viral diseases, pain
 CC disorders, metabolic disorders, neurological or central nervous system
 CC disorders, erythroid disorders, blood vessel disorders or angiogenic
 CC disorders (all claimed), e.g. cancer, heart failure, hypertension,
 CC angina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, Crohn's
 CC disease, psoriasis, or asthma. The nucleic acid molecules and
 CC polypeptides are also useful as modulating agents in regulating a variety
 CC of cellular process, e.g. cell proliferation, differentiation, growth and
 CC division. This is the amino acid sequence of a novel human protein of the
 CC invention. Note: The sequences given in the specification are also
 CC available in electronic format from
 CC ftp.segdata.uspto.gov/sequence.html?DocID=20040058355.
 XX
 SQ Sequence 778 AA;

Query Match 87.4%; Score 3545; DB 8: Length 778;
 Best Local Similarity 99.7%; Pred. No. 6.9e-235;
 Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	89	FRYLVLVHVGSGGLFDYLVKKGLTPEAKRFRQIVSALDFCHSYICHRLDKPENLLL	148
Db	105	YLYLVHVGSGGLFDYLVKKGLTPEAKRFRQIVSALDFCHSYICHRLDKPENLLL	164
Qy	149	DEKNIRIADFGMASLQVGSLLTSCGSHYACPEVIGKGYDGRADMMSCGVILPAL	208
Db	165	DEKNIRIADFGMASLQVGSLLTSCGSHYACPEVIGKGYDGRADMMSCGVILPAL	224
Qy	209	LVGALPDDDLNQLLEKVRGVFHPHFIPPCQSLLRGMIEVEPEKRLSLEQIQKHPW	268
Db	225	LVGALPDDDLNQLLEKVRGVFHPHFIPPCQSLLRGMIEVEPEKRLSLEQIQKHPW	284
Qy	269	YLGKKEPDPCLPEPAPGRRVAMRSLPSNGELDPDVLSEMASLGCFRDRRLHRLSEEE	328
Db	285	YLGKKEPDPCLPEPAPGRRVAMRSLPSNGELDPDVLSEMASLGCFRDRRLHRLSEEE	344
Qy	329	NOEKMIYLLLDKRYPCSCDQDLPPRNDVDPKRVDSFPMLSRHGKRPERKSMVLS	388
Db	345	NOEKMIYLLLDKRYPCSCDQDLPPRNDVDPKRVDSFPMLSRHGKRPERKSMVLS	404
Qy	389	ITDAGGGSPVPTTRALEMAHQSRSSVSGASTGLSSSLSPSPRSVFSPEPGAGDE	448
Db	405	ITDAGGGSPVPTTRALEMAHQSRSSVSGASTGLSSSLSPSPRSVFSPEPGAGDE	464
Qy	449	ARGGGPTSKTQTLPSRGRGGGAGEOPPPPSARSTPLPGPPSPRSSGGTPLHSLHTP	508
Db	465	ARGGGPTSKTQTLPSRGRGGGAGEOPPPPSARSTPLPGPPSPRSSGGTPLHSLHTP	524
Qy	509	RASPTGTPGTPPPSPGGVGGAAWRSLRSLRNSFLGSRFHRKRNQVPTAEEMSLTP	568
Db	525	RASPTGTPGTPPPSPGGVGGAAWRSLRSLRNSFLGSRFHRKRNQVPTAEEMSLTP	584
Qy	569	ESSPELAKRSWFGNFIISLDEEQIFLVLDKDKPLSSIKADIVHAFSLTSPSLSHSVLSQTSF	628
Db	585	ESSPELAKRSWFGNFIISLDEEQIFLVLDKDKPLSSIKADIVHAFSLTSPSLSHSVLSQTSF	644
Qy	629	RAYKASGGSPVFKPVRFOVDISSSEGGPSPRRDGGGGGGIYSVFTTILSGPSRFRKR	688
Db	645	RAYKASGGSPVFKPVRFOVDISSSEGGPSPRRDGGGGGGIYSVFTTILSGPSRFRKR	704
Qy	689	VWTIOAQLLSTHDQPSVQALADENKGAQTRPAGAPRRSLQPPGPDPELSSSPRRGPP	748
Db	705	VWTIOAQLLSTHDQPSVQALADENKGAQTRPAGAPRRSLQPPGPDPELSSSPRRGPP	764
Qy	749	KDKKLLATNGTPLP 762	

FT	Domain	34..286	/note = Tyrosine kinase domain	1	
FT	Domain	34..285	/note = Eukaryotic protein kinase domain		
FT	Domain	152..164	/note = Serine/threonine kinase domain		
FT	Modified-site	208..211	/note = "Amidation site"		
FT	Domain	214..231	/note = Transmembrane domain		
FT	Modified-site	300..303	/note = "Amidation site"		
FT	Domain	315..356	/note = UBA domain		
FT	Modified-site	390..393	/note = "Amidation site"		
FT	Binding-site	682..685	/note = "Glycosaminoglycan attachment site"		
XX	US6787345-B1.				
XX	07-SEP-2004.				
XX	15-NOV-2001; 2001US-00003690.				
XX	15-NOV-2000; 2000US-0248893P.				
XX	(MILL-) MILLENNIUM PHARM INC.				
XX	Curtis RAJ;				
XX	WPI; 2004-632931/61.				
XX	N-PSDB; ADS16425, ADS16427, ADS16433.				
XX	New isolated eukaryotic kinase (EPK-55053) nucleic acid and protein,				
XX	useful for diagnosing or treating EPK-55053 mediated or related				
XX	disorders, e.g. Alzheimer's disease, multiple sclerosis, depression,				
XX	ischemia, restenosis, or diabetes.				
XX	Claim 2; SEQ ID NO 2; 55pp; English.				
XX	The invention relates to an eukaryotic protein kinase-55053 (EPK-55053)				
XX	and its corresponding nucleic acid sequence. The EPK-55053 nucleic acid				
XX	molecules, proteins and antibodies are useful in screening assays,				
XX	diagnostic assays, prognostic assays, in monitoring clinical trials,				
XX	pharmacogenetics or for treating EPK-55053 mediated or related disorders.				
XX	EPK-55053 mediated or related disorders include CNS disorders				
XX	(Alzheimer's disease, Parkinson's disease, multiple sclerosis,				
XX	amyotrophic lateral sclerosis or epilepsy), autonomic function disorders				
XX	(sleep disorders, depression, mania, anxiety disorders or phobic				
XX	disorders), learning or memory disorders (amnesia or attention deficit				
XX	disorder), cardiovascular system disorders (arteriosclerosis, ischaemia,				
XX	reperfusion injury, restenosis or vascular heart disease), hormonal				
XX	disorders (diabetes or thyroid disorders) and reproductive or fertility				
XX	disorders. The present sequence is human EPK-55053 enzyme.				
XX	Sequence 778 AA;				
XX	Query Match	87.4%;	Score 3545;	DB 8;	Length 778;
XX	Best Local Similarity	99.7%;	Pred. No. 6.9e-235;		
XX	Matches 672; Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;	
Qy	89	FRYLVEHVSQGEFLDYLVKKGRITPKAEKFFRQIVSALDFCHSYICHRLDKPENLLL	148		
Db	105	YLXVLVEHVSQGEFLDYLVKKGRITPKAEKFFRQIVSALDFCHSYICHRLDKPENLLL	164		
Qy	149	DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADMMSCVILFAL	208		
Db	165	DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADMMSCVILFAL	224		
Qy	209	LVGALPDDNNLRQLLEKVRGVFMPHFIPDCQSLLRGMIEVEPEKRLSLEIQKHPW	268		
Db	225	LVGALPDDNNLRQLLEKVRGVFMPHFIPDCQSLLRGMIEVEPEKRLSLEIQKHPW	284		
Qy	269	YLGKHEPDPCLPEPAPGRRVAMRSLPSNGELDDPVLESMAISLGCFRDRERLHRLRSEE	328		
Db	285	YLGKHEPDPCLPEPAPGRRVAMRSLPSNGELDDPVLESMAISLGCFRDRERLHRLRSEE	344		
Qy	329	NOEKMIYLLLDKRYPCEDODLPPRNDVDPKRVDSFPMLSHGKRRRPERKSMVLS	388		
Db	345	NOEKMIYLLLDKRYPCEDODLPPRNDVDPKRVDSFPMLSHGKRRRPERKSMVLS	404		
Qy	389	ITDAGGGSPVPTTRALEMAQHSQSRSSVSGASTGLSSPLSSPRSPVFSFSPFGAGDE	448		
Db	405	ITDAGGGSPVPTTRALEMAQHSQSRSSVSGASTGLSSPLSSPRSPVFSFSPFGAGDE	464		
Qy	449	ARGGSPSTKTQTLPSRPGGAGGEPSPSARSTPLPGPPSPRSGGTPLHSLHTP	508		
Db	465	ARGGSPSTKTQTLPSRPGGAGGEPSPSARSTPLPGPPSPRSGGTPLHSLHTP	524		
Qy	509	RASPTGTPGTTPPPSPGGVGGAAWRSLRSLRNSIRNSFLGSPFRHRRKMQVPTAEMSSLTP	568		
Db	525	RASPTGTPGTTPPPSPGGVGGAAWRSLRSLRNSIRNSFLGSPFRHRRKMQVPTAEMSSLTP	584		
Qy	569	ESSPELAKRSMFNGNIFSLDKKEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF	628		
Db	585	ESSPELAKRSMFNGNIFSLDKKEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF	644		
Qy	629	RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGGIYSVTFTLISGSRAPKR	688		
Db	645	RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGGIYSVTFTLISGSRAPKR	704		
Qy	689	VVETIQALLSTHDQPSVQALADEKKAQTRPAGAPPRSLQPPGPRDPELSSSPRGPP	748		
Db	705	VVETIQALLSTHDQPSVQALADEKKAQTRPAGAPPRSLQPPGPRDPELSSSPRGPP	764		
Qy	749	KDKKLLATNGTPLP	762		
Db	765	KDKKLLATNGTPLP	778		
XX	RESULT 11				
XX	AAU03517				
XX	ID AAU03517 standard; protein; 794 AA.				
XX	AC AAU03517;				
XX	DT 12-SEP-2001 (first entry)				
XX	DE Human protein kinase #17.				
XX	XX Human; protein kinase; PK; STK; cancer; cardiovascular disease;				
XX	XX metabolic disorder; immune related disease; neurological disorder;				
XX	XX neurodegenerative disorder; inflammatory disorder; infectious disease;				
XX	XX reproductive disorder.				
XX	OS Homo sapiens.				
XX	XX WO200138503-A2.				
XX	XX 31-MAY-2001.				
XX	XX 22-NOV-2000; 2000WO-US032085.				
XX	XX 24-NOV-1999; 99US-0167482P.				
XX	XX (SUGE-) SUGEN INC.				
XX	XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;				
XX	XX Flanagan P, Clary D;				
XX	XX WPI; 2001-343950/36.				
XX	XX N-PSDB; AAS06717.				
XX	XX Nucleic acids encoding human kinase polypeptides, useful for preventing				
XX	XX diagnosing and/or treating e.g. cancer, immune, cardiovascular and				

PT	neuronal-associated diseases, and microbial infections.
XX	Claim 7; Fig 2; 433pp; English.
XX	AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
PS	protein kinases have been identified as members of the tyrosine or
XX	serine/threonine kinase (PTK and STK) families. The polynucleotides
CC	encoding protein kinases and the polypeptides may be used in the
CC	prevention, diagnosis and treatment of diseases associated with
CC	inappropriate kinase expression. For example, they may be used to treat
CC	cancers (especially cancers of haematopoietic origin), cardiovascular
CC	disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC	immune related diseases (e.g. rheumatoid arthritis), neurological
CC	disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC	Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC	disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC	Additionally, polynucleotides encoding protein kinases may be used for
CC	gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC	polypeptides may be used as antigens in the production of antibodies
CC	against the protein kinases and in assays to identify modulators of
CC	protein kinase expression and activity
XX	Sequence 794 AA;
SQ	Query Match 87.4%; Score 3545; DB 4; Length 794;
	Best Local Similarity 99.7%; Pred. No. 7.1e-235;
	Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	89 FRYLVLEHVGSGELFDYLVKKGRLTPKEARFFQIVSALDFCHSYISCHRDLPENLLL 148
DB	121 YLYLVLEHVGSGELFDYLVKKGRLTPKEARFFQIVSALDFCHSYISCHRDLPENLLL 180
QY	149 DEKNIRIADFGMASLQVDSLLSTSCGSHYACPEVVKGEYDGRADMWSCVILFAL 208
DB	181 DEKNIRIADFGMASLQVDSLLSTSCGSHYACPEVVKGEYDGRADMWSCVILFAL 240
QY	209 LVGALPFDDNLRQLLEKRVGVFHMHPFIIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 268
DB	241 LVGALPFDDNLRQLLEKRVGVFHMHPFIIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 300
QY	269 YLGGKHEPDCLEPAPGRVAMRSLPSNGELDDPVLESMSLGCGRFRERLHRLSEEE 328
DB	301 YLGGKHEPDCLEPAPGRVAMRSLPSNGELDDPVLESMSLGCGRFRERLHRLSEEE 360
QY	329 NOEKMIYLLLDKREYKSCEDQDLPFRNDVDPKRVDSPLMRHGRKRRPERKSMEYLS 388
DB	361 NOEKMIYLLLDKREYKSCEDQDLPFRNDVDPKRVDSPLMRHGRKRRPERKSMEYLS 420
QY	389 ITDAGGGSPVPTRRALEMAQHSQSRSVSGASTGLSSPLSSPRSPVFSFSPFGAGDE 448
DB	421 ITDAGGGSPVPTRRALEMAQHSQSRSVSGASTGLSSPLSSPRSPVFSFSPFGAGDE 480
QY	449 ARGGSPTSQTTLSPRGGGAGCEQPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 508
DB	481 ARGGSPTSQTTLSPRGGGAGCEQPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 540
QY	509 RASPTGTPTCTPPPPGGGVGGAARSLNRNSFLGSPRFRHKKMQVPTAEEMSSLTP 568
DB	541 RASPTGTPTCTPPPPGGGVGGAARSLNRNSFLGSPRFRHKKMQVPTAEEMSSLTP 600
QY	569 ESSPELAKSWFGNFTSLDKERQIFLVLDKPLSSIKADIVHAFSLISLHSLVLSQTSF 628
DB	601 ESSPELAKSWFGNFTSLDKERQIFLVLDKPLSSIKADIVHAFSLISLHSLVLSQTSF 660
QY	629 RAEYKASGSPVQKRVQVDIISSEGEPPPRDGGGGGIYSVTFTLISGPPRRFRK 688
DB	661 RAEYKASGSPVQKRVQVDIISSEGEPPPRDGGGGGIYSVTFTLISGPPRRFRK 720
QY	689 VVETIQALLSTHDQPSVALADEKNQAOTRPAQAPRPSLOPPGPPDELSSSPRRGPP 748
DB	721 VVETIQALLSTHDQPSVALADEKNQAOTRPAQAPRPSLOPPGPPDELSSSPRRGPP 780
QY	749 KDKKLLATNGTPLP 762

DB	781 KDKKLLATNGTPLP 794
RESULT 12	
AAE16271	
ID	AAE16271 standard; protein; 794 AA.
XX	AAE16271;
AC	AAE16271;
XX	26-MAR-2002 (first entry)
DE	Human kinase PKIN-17 protein.
XX	Human; kinase; PKIN-17; cancer; leukaemia; adenocarcinoma; osteoporosis;
KW	immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW	Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW	allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW	autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
KW	Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW	rheumatoid arthritis; ulcerative colitis; cirrhosis; angina pectoris;
KW	hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW	cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW	congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW	fatty liver; Niemann-Pick's disease; gene therapy.
XX	Homo sapiens.
OS	
XX	
PH	Key
FT	Domain
FT	Domain
FT	Domain
FT	Domain
FT	Domain
FT	Domain
FT	Domain
XX	W0200196547-A2.
XX	20-DEC-2001.
XX	14-JUN-2001; 2001WO-US019444.
XX	15-JUN-2000; 2000US-0212073P.
PR	23-JUN-2000; 2000US-0213467P.
PR	30-JUN-2000; 2000US-0215651P.
PR	07-JUL-2000; 2000US-0216605P.
PR	13-JUL-2000; 2000US-0218372P.
PR	25-AUG-2000; 2000US-0228056P.
XX	(INCY-) INCYTE GENOMICS INC.
XX	Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
XX	Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;
PI	Rankumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YF;
PI	Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
PI	Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
PI	Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
XX	WPI; 2002-090207/12.
DR	N-PSDB; AAD26464.
XX	New polypeptides, useful for diagnosing, treating or preventing disorders
PT	of growth and development, cardiovascular and lipid, and diseases such as
PT	cancer, comprise human kinase polypeptides.
XX	Claim 1; Page 159-161; 197pp; English.
PS	The invention relates to human kinase PKIN proteins and their
CC	corresponding cDNAs. A composition containing PKIN agonist is useful for
CC	treating a disease or condition associated with decreased expression of
CC	PKIN and a composition comprising PKIN antagonist is useful for treating

a disease or condition associated with overexpression of PKIN. The disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, atherosclerosis, anaemia, allergies, adult respiratory distress syndrome, autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease, osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis, bacterial, parasitic, fungal, viral, protozoal and helminthic infections) growth and development disorders (arteriosclerosis, cirrhosis, hepatitis, Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio vascular disease (arteriovenous fistula, hypertension, vasculitis, aneurysms, congestive heart failure, angina pectoris, myocarditis, ischaemic heart disease, chronic bronchitis, lung tumours); lipid disorder (fatty liver, Fabry's disease, Niemann-Pick's disease, hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity of a test compound and in gene therapy. The present sequence is human PKIN-17 protein

XX SQ Sequence 794 AA;

Query Match 87.4%; Score 3545; DB 5; Length 794;
 Best Local Similarity 99.7%; Pred. No. 7.1e-235;
 Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 89 FRYLVLEHVS GGELFDYLVKKGRLLTPKEARKFRQIVSALDFCHSYSTCHRDLPENLL 148
 Db : |||||
 121 YLYLVLEHVS GGELFDYLVKKGRLLTPKEARKFRQIVSALDFCHSYSTCHRDLPENLL 180
 Qy 149 DEKNIRIADFGMASLQVDSLLTSCGSHYACPEVIKGEYDGRADWMSCGVILPAL 208
 Db |||||
 181 DEKNIRIADFGMASLQVDSLLTSCGSHYACPEVIKGEYDGRADWMSCGVILPAL 240
 Qy 209 LVGALPPDDNNLRQLLEKVRGVFHPHFIPDQCQLLRGMIEVEPEKRLSLEQIQHPW 268
 Db |||||
 241 LVGALPPDDNNLRQLLEKVRGVFHPHFIPDQCQLLRGMIEVEPEKRLSLEQIQHPW 300
 Qy 269 YLGKKEHPDPCLEPAPGRVAMRSLPSNGELDPDVLESMAISGCFRDRERLHRELSEEE 328
 Db |||||
 301 YLGKKEHPDPCLEPAPGRVAMRSLPSNGELDPDVLESMAISGCFRDRERLHRELSEEE 360
 Qy 329 NQEKMIYLLLDKREYFPCEDQDLPNRNDVDPKRVDSMLSRHGKRRPERKSMVLS 388
 Db |||||
 361 NQEKMIYLLLDKREYFPCEDQDLPNRNDVDPKRVDSMLSRHGKRRPERKSMVLS 420
 Qy 389 ITDAGGGGSPVPTTRALEMAHQSRSVSGASTGLSSPLSSPRSPVFSFSPGAGDE 448
 Db |||||
 421 ITDAGGGGSPVPTTRALEMAHQSRSVSGASTGLSSPLSSPRSPVFSFSPGAGDE 480
 Qy 449 ARGGSPSTKTQTLPSRGRGGGAGEQPPPSARSTPLPGPPSPRSSGGTPLHSLHTP 508
 Db |||||
 481 ARGGSPSTKTQTLPSRGRGGGAGEQPPPSARSTPLPGPPSPRSSGGTPLHSLHTP 540
 Qy 509 RASTGTGPTTTPPSPGGVGGAWRSLNIRNSFLGSPRFRKMQVPTAEEMSLTP 568
 Db |||||
 541 RASTGTGPTTTPPSPGGVGGAWRSLNIRNSFLGSPRFRKMQVPTAEEMSLTP 600
 Qy 569 ESSPELAKRSWFGNFISLDKEQIFLVLDKPLSSIADIVHAFISIPSLSHSVLSQTSF 628
 Db |||||
 601 ESSPELAKRSWFGNFISLDKEQIFLVLDKPLSSIADIVHAFISIPSLSHSVLSQTSF 660
 Qy 629 RAEYKASGGSPVKPVRQVDIISSESGPEPSRRDGGSGGGIYSVFTLISGSRFRK 688
 Db |||||
 661 RAEYKASGGSPVKPVRQVDIISSESGPEPSRRDGGSGGGIYSVFTLISGSRFRK 720
 Qy 689 VVETIQALLSTHQPVSQALADEKNGAQTRPAGAPRSLQPPGRDPDELSSSPRRGPP 748
 Db |||||
 721 VVETIQALLSTHQPVSQALADEKNGAQTRPAGAPRSLQPPGRDPDELSSSPRRGPP 780
 Qy 749 KDKKLLATNGTPLP 762
 Db |||||
 781 KDKKLLATNGTPLP 794

RESULT 13
AA016604

ID AA016604 standard; protein; 754 AA.

XX AC AA016604;

XX DT 08-MAY-2003 (first entry)

XX DE Human cell cycle-regulatory factor Cdr2.

XX KW Human; cell cycle-regulatory factor; Cdr2; kinase; proliferative disease;
 XX KW anticancer agent; wound-healing drug.

XX OS Homo sapiens.

XX PN WO200299110-A1.

XX PD 12-DEC-2002.

XX PF 03-JUN-2002; 2002WO-JF005411.

XX PR 04-JUN-2001; 2001JP-00168792.

XX PA (TAIH) TAIHO PHARM CO LTD.

XX PA (NAKA/) NAKANISHI M.

XX PI Nakanishi M;

XX DR WPI; 2003-156857/15.

XX DR N-PSDB; AAL51889.

XX PT Cell cycle-regulatory factor Cdr2 with kinase activity and encoded gene,
 XX PT applicable in diagnosis of and screening drugs for proliferative diseases
 XX PT e.g. anticancer agents and wound-healing drugs.

XX PS Claim 1; Fig 2 A-C; 63pp; Japanese.

XX CC The invention comprises the amino acid and coding sequence of the human
 XX CC cell cycle-regulatory factor Cdr2 (with kinase activity). The DNA and
 XX CC protein sequences of the invention are useful in diagnosing and screening
 XX CC drugs for proliferative diseases (e.g. anticancer agents and wound-
 XX CC healing drugs). The present amino acid sequence represents the human cell
 XX CC cycle-regulatory factor Cdr2 protein

XX SQ Sequence 754 AA;

Query Match 82.9%; Score 3362; DB 6; Length 754;
 Best Local Similarity 95.4%; Pred. No. 2.5e-222;
 Matches 643; Conservative 1; Mismatches 6; Indels 24; Gaps 1;

Qy 89 FRYLVLEHVS GGELFDYLVKKGRLLTPKEARKFRQIVSALDFCHSYSTCHRDLPENLL 148
 Db : |||||
 105 YLYLVLEHVS GGELFDYLVKKGRLLTPKEARKFRQIVVVCAGLCHSYSTCHRDLPENLL 164
 Qy 149 DEKNIRIADFGMASLQVDSLLTSCGSHYACPEVIKGEYDGRADWMSCGVILPAL 208
 Db |||||
 165 DEKNIRIADFGMASLQVDSLLTSCGSHYACPEVIKGEYDGRADWMSCGVILPAL 224
 Qy 209 LVGALPPDDNNLRQLLEKVRGVFHPHFIPDQCQLLRGMIEVEPEKRLSLEQIQHPW 268
 Db |||||
 225 LVGALPPDDNNLRQLLEKVRGVFHPHFIPDQCQLLRGMIEVEPEKRLSLEQIQHPW 284
 Qy 269 YLGKKEHPDPCLEPAPGRVAMRSLPSNGELDPDVLESMAISGCFRDRERLHRELSEEE 328
 Db |||||
 285 YLGKKEHPDPCLEPAPGRVAMRSLPSNGELDPDVLESMAISGCFRDRERLHRELSEEE 344
 Qy 329 NQEKMIYLLLDKREYFPCEDQDLPNRNDVDPKRVDSMLSRHGKRRPERKSMVLS 388
 Db |||||
 345 NQEKMIYLLLDKREYFPCEDQDLPNRNDVDPKRVDSMLSRHGKRRPERKSMVLS 404
 Qy 389 ITDAGGGGSPVPTTRALEMAHQSRSVSGASTGLSSPLSSPRSPVFSFSPGAGDE 448

Db 405 ITDAGGGSPVTRRALEMAQHSQSRVSGASTGLSSPLSSPRSPVFSPEPGAGDE 464
Qy 449 ARGGSPTSXTOTLPSRGRGGAGQPPPSARSTPLPGPGSPRSSGGTPLHSPHTP 508
Db 465 ARGGSPTSXTOTLPSRGRGGAGQPPPSARSTPLPGPGSPRSSGGTPLHSPHTP 500
Qy 509 RASPTGPTTTPPPSGGAGAAWRLNSIRNSFLGSPRFRHRRKQVPTAEEMSSLTP 568
Db 501 RASPTGPTTTPPPSGGAGAAWRLNSIRNSFLGSPRFRHRRKQVPTAEEMSSLTP 560
Qy 569 ESSPELAKRWGFIQLDKEQIFLVLDKPLSSIKADIVHAFLSIPSLSHSVLSQTSF 628
Db 561 ESSPELAKRWGFIQLDKEQIFLVLDKPLSSIKADIVHAFLSIPSLSHSVLSQTSF 620
Qy 629 RAEYKASGSPVFOKPVRFQVDSISSEGPSPRRDGGGGGIYSVTFTLISGFSRRFKR 688
Db 621 RAEYKASGSPVFOKPVRFQVDSISSEGPSPRRDGGGGGIYSVTFTLISGFSRRFKR 680
Qy 689 VVETIQALLSTHDQPSVQALADEKGAQTRPAGAPPSLQPPGRDPPELSSSPRRGPP 748
Db 681 VVETIQALLSTHDQPSVQALADEKGAQTRPAGAPPSLQPPGRDPPELSSSPRRGPP 740
Qy 749 KKKLLATNGTPLP 762
Db 741 KKKLLATNGTPLP 754

RESULT 14
ADQ65624 standard; protein; 473 AA.
AC ADQ65624;
XX 07-OCT-2004 (first entry)
XX Novel human protein sequence #597.
DE osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
XX gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX Homo sapiens.
XX EP1440981-A2.
XX 28-JUL-2004.
XX 21-JAN-2004; 2004EP-00001196.
XX 21-JAN-2003; 2003JP-00102206.
XX 09-MAY-2003; 2003JP-00131392.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Negai K, Irie R;
XX WPI; 2004-535376/52.
XX N-PSDB; ADQ63436.
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX Claim 1; SEQ ID NO 2785; 2449pp; English.
XX The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,

CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a protein
CC sequence of the invention.
XX Sequence 473 AA;
Query Match 60.8%; Score 2467; DB 8; Length 473;
Best Local Similarity 99.8%; Pred. No. 4.8e-161;
Matches 472; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 290 MRSPLPSNGELDPDVLSEWASIGCFRDERLHRELSEENQEKMIYLLLDKRYEVSCE 349
Db 1 MRSPLPSNGELDPDVLSEWASIGCFRDERLHRELSEENQEKMIYLLLDKRYEVSCE 60
Qy 350 DODLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLSITDAGGGSPVPTRALEMAQ 409
Db 61 DODLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLSITDAGGGSPVPTRALEMAQ 120
Qy 410 HSQRSRSVSGASTGLSSPLSSPRSPVFSPEPGAGDEARGGSPSTKTTLPSRGRPG 469
Db 121 HSQRSRSVSGASTGLSSPLSSPRSPVFSPEPGAGDEARGGSPSTKTTLPSRGRPG 180
Qy 470 CGAGQPPPPSARSTPLPGPGSPRSSGGTPLHSPHTPRASTGTCTTTPPPSGGGVG 529
Db 181 CGAGQPPPPSARSTPLPGPGSPRSSGGTPLHSPHTPRASTGTCTTTPPPSGGGVG 240
Qy 530 GAAWRLNSIRNSFLGSPRFRHRRKQVPTAEEMSSLTPSESPPELAKRWGFIQLDKE 589
Db 241 GAAWRLNSIRNSFLGSPRFRHRRKQVPTAEEMSSLTPSESPPELAKRWGFIQLDKE 300
Qy 590 EQIFLVLDKPLSSIKADIVHAFLSIPSLSHSVLSQTSFRAEYKASGSPVFOKPVRFQV 649
Db 301 EQIFLVLDKPLSSIKADIVHAFLSIPSLSHSVLSQTSFRAEYKASGSPVFOKPVRFQV 360
Qy 650 DISSEGEPPSPRRDGGGGGIYSVTFTLISGFSRRFKRVVETIQALLSTHDQPSVQAL 709
Db 361 DISSEGEPPSPRRDGGGGGIYSVTFTLISGFSRRFKRVVETIQALLSTHDQPSVQAL 420
Qy 710 ADEKGAQTRPAGAPPSLQPPGRDPPELSSSPRRGPPKDKLLATNGTPLP 762
Db 421 ADEKGAQTRPAGAPPSLQPPGRDPPELSSSPRRGPPKDKLLATNGTPLP 473

RESULT 15
ADR50797 standard; protein; 766 AA.
XX ADR50797;
XX 18-NOV-2004 (first entry)
XX Human c-bramy3018357 protein kinase SeqID 20.
XX human; enzyme; kinase; screening method; hepatic carcinoma; renal cancer;
XX testis cancer; hepatitis; liver cirrhosis; nephritis; diabetes;
XX inflammatory disease.
XX Homo sapiens.
XX WO2004074485-A1.
XX 02-SEP-2004.
XX 24-FEB-2004; 2004WO-JP002133.
XX 24-FEB-2003; 2003JP-00046606.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX (ZOBG-) ZOEGENE CORP.
XX Isogai T, Sugiyama T, Wakamatsu A, Irie R, Ishii S, Kawai K;
PI Kajii T, Nakajima M, Miyama N, Kishimoto T, Kondo J;
XX

DR WPI: 2004-652962/63.
DR N-PSDB; ADR50785.
XX Novel protein having kinase activity, useful for diagnosing diseases e.g.
PT hepatic carcinoma, renal cancer, testis cancer, hepatitis, liver
PT cirrhosis, nephritis, diabetes or inflammatory disease.
XX
PS Claim 1; SEQ ID NO 20; 288pp; Japanese.
XX
CC This invention relates to novel isolated nucleic acid molecules that
CC encode proteins with a kinase activity. Specifically, it refers to the
CC analysis of cDNA clones contained within a full length cDNA library and
CC the identification of the physiological activity of the encoded protein
CC thereof. The present invention describes a recombinant vector and host
CC cell for expression of the nucleic acids of interest, as well as
CC antisense oligos and antibodies that can be used to modulate expression
CC and neutralise kinase activity respectively. In particular, these
CC proteins can be used for screening regulatory substances in order to
CC detect and measure a change in kinase activity. Accordingly, these can be
CC developed into pharmaceutical compositions that are useful for diagnosing
CC diseases such as hepatic carcinoma, renal cancer, testis cancer,
CC hepatitis, liver cirrhosis, nephritis, diabetes or inflammatory disease.
CC This polypeptide sequence is an exemplary human kinase protein of the
CC invention.
XX
SQ Sequence 766 AA;
Query Match 59.2%; Score 2400; DB 8; Length 766;
Best Local Similarity 68.5%; Pred. No. 3.5e-156;
Matches 475; Conservative 59; Mismatches 65; Indels 94; Gaps 10;
QY 89 FRYLVLEHVSQGEFLDYLVKKGRITPKKARFFQIVSALDFCHSYICHRLDKPENLLL 148
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 136
YLVLVLEHVSQGEFLDYLVKKGRITPKKARFFQIIISALDFCHSHICHRLDKPENLLL 195
QY 149 DEKNRIADFGMASLQVDSLLTSCGSPHYACPEVTKGKYDGRADMWCGVILFAL 208
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 196
DEKNRIADFGMASLQVDSLLTSCGSPHYACPEVIRGEKYDGRKADVWSCGVILFAL 255
QY 209 LVGALPFDDNNLRQLLEKVRGVFHPHFIPDCQSLLRGMIEVEPEKRLSLEQIORHPW 268
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 256
LVGALPFDDNNLRQLLEKVRGVFHPHFIPDCQSLLRGMIEVDAAARLTLEHIQHHW 315
QY 269 YLGKKEPDPCLPEPAGRRVAMRSLPSNGELDPVLESMAISLGCGRDRERLHRLRSEEE 328
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 316
YIGKNEPEP-EQIP-P-KVQIRSLPSLEDIDPDVLSMHSGLGCFDRNKLQDLLSEEE 373
QY 329 NOEKMIYLLLDKRYPSCEDQLPRNDVDPKRVDSPLMSHGKRRPERKSMVLS 388
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 374
NOEKMIYLLLDKRYPSQEDQLPRNEIDPPKRVDSPLMNRHGRKRRPERKSMVLS 433
QY 389 ITDAGGGGSPVPTRRALMAHQSRSVSGASTGLSSPLSSPSRSPVFSPEPGAGDE 448
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 434
VTD---GGSPVARRAIEAHHQGRSRSISGASSGLSTSLSSPR----- 475
QY 449 ARGCGSPSTKTQTLPSRGGGAGEOPPPPSARSTPLPGPGSPRSGGTFPLHSPLHTP 508
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 476
-----VTPHPSRGSPLTPKG-----TPVHTP 498
QY 509 RASPTGTGTTTPPSGGVGAARSLNLSIRNSFLGSPFRHRRKMQVPTAEEMSSILTP 568
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 499
KESPAFTNPTPPSSP--SVGGVPWRLNLSIRNSFLGSPFRHRRKMQVPTPEEMSNLTP 556
QY 569 ESSPELAKRSWFGNFISLDKEEQIFVLKDKKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 557
ESSPELAKRSWFGNFISLEKEEQIFVVKDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 616
QY 629 RAEYKASGGSPVQKVRQVDIISSESGPEPSPRDGGGGIYSVFTTLISGSPRRFKR 688
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 617
RAEYKATGGPAVQKVRQVDIYVTEGGEAQKE-----NGIYSVFTTLISGSPRRFKR 670
QY 689 VVETIQALLSTHDPQSVQALA-----DEKNGAQTRPAGAPPR----- 726
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 671 VVETIQALLSTHDPQSVQALA-----DEKNGAQTRPAGAPPR----- 730
QY 727 -----SLQPPPG--RPDPSELSSSPRRGPPKDKK 752
Db 731 LGDSAAAGPGGDAEYPTGKDTAKMGPTARR 763
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Job time : 183 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 10:39:03 ; Search time 47 Seconds
(without alignments)
1210.268 Million cell updates/sec

Title: US-10-803-277-4

Perfect score: 4056

Sequence: 1 MGLEFGFLEAGGNWSHPLG.....PRRGPPKDKLLATNGTFLP 762

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4056	100.0	762	4	US-10-116-326-4
2	3545	87.4	703	4	US-10-116-326-6
3	3545	87.4	778	4	US-10-116-326-2
4	3545	87.4	778	4	US-10-003-690-2
5	2390.5	58.9	585	4	US-09-930-181-4
6	2386.5	58.8	668	4	US-09-930-181-2
7	2381.5	58.7	603	4	US-09-930-181-17
8	637	15.7	691	4	US-09-949-016-8255
9	637	15.7	691	4	US-09-949-016-8256
10	636	15.7	724	4	US-09-984-890-2
11	636	15.7	724	4	US-10-274-194-2
12	636	15.7	745	4	US-09-523-849-36
13	631	15.6	722	4	US-09-984-890-4
14	631	15.6	722	4	US-10-274-194-4
15	629	15.5	722	4	US-08-817-832B-32
16	610	15.0	724	4	US-09-949-016-8234
17	608	15.0	713	4	US-09-538-092-1022
18	608	15.0	713	4	US-09-949-016-6214
19	606	14.9	729	2	US-08-677-298-2
20	606	14.9	729	4	US-09-523-849-33
21	604	14.9	776	4	US-09-523-849-34
22	603.5	14.9	602	4	US-09-949-016-7417
23	603.5	14.9	602	4	US-09-949-016-7418
24	602	14.8	1203	4	US-09-799-875-5
25	595	14.7	793	4	US-09-523-849-32
26	593	14.6	511	4	US-09-633-328B-4
27	589	14.5	511	4	US-09-633-328B-2

28	579	14.3	149	4	US-09-930-181-18	Sequence 18, Appl
29	577.5	14.2	779	4	US-08-817-832B-31	Sequence 31, Appl
30	569.5	14.0	360	4	US-09-248-796A-20497	Sequence 20497, A
31	564	13.9	915	4	US-09-538-092-63	Sequence 63, Appl
32	551.5	13.6	557	4	US-09-949-016-10174	Sequence 10174, A
33	548.5	13.5	552	4	US-09-538-092-1212	Sequence 1212, Ap
34	548.5	13.5	552	4	US-09-824-735-4	Sequence 4, Appli
35	545.5	13.4	521	4	US-09-949-016-7570	Sequence 7570, Ap
36	542.5	13.4	552	3	US-08-557-006C-40	Sequence 40, Appl
37	541	13.3	633	3	US-08-557-006C-43	Sequence 43, Appl
38	541	13.3	633	4	US-09-538-092-1212	Sequence 212, App
39	541	13.3	633	4	US-09-633-328B-3	Sequence 3, Appli
40	541	13.3	633	4	US-09-824-735-3	Sequence 3, Appli
41	539.5	13.3	345	3	US-09-101-146-1	Sequence 1, Appli
42	533	13.1	257	3	US-09-101-146-6	Sequence 6, Appli
43	531.5	13.1	604	4	US-09-523-849-35	Sequence 35, Appl
44	502.5	12.4	418	4	US-09-248-796A-18441	Sequence 18441, A
45	494.5	12.2	257	2	US-07-857-224B-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-10-116-326-4

; Sequence 4, Application US/10116326

; Patent No. 6777545

; GENERAL INFORMATION:

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Mathur, Brian

; APPLICANT: Friddle, Carl Johan

; TITLE OF INVENTION: No. 6777545el Human Kinases and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0332-USA

; CURRENT APPLICATION NUMBER: US/10/116,326

; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/282,036

; PRIOR FILING DATE: 2001-04-06

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 762

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-116-326-4

Query Match 100.0%; Score 4056; DB 4; Length 762;
Best Local Similarity 100.0%; Pred. No. 5.7e-266;
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGLEFGFLEAGGNWSHPLPGSDGNWNLFLPGINGNWSLFLPGTHGNWSLFLPRIMGIGVL	60
Db	1	MGLEFGFLEAGGNWSHPLPGSDGNWNLFLPGINGNWSLFLPGTHGNWSLFLPRIMGIGVL	60
Qy	61	CHQPEVVGDEALWSSSTCPQSPAPSSIFRYLVLEHVSGGELFDYLVKKGRLTPKEARKF	120
Db	61	CHQPEVVGDEALWSSSTCPQSPAPSSIFRYLVLEHVSGGELFDYLVKKGRLTPKEARKF	120
Qy	121	FRQIVSALDFCHSYISICHRDLKPENLLDKNNIRIADFGWASLQVGSLLLETSCGSPHY	180
Db	121	FRQIVSALDFCHSYISICHRDLKPENLLDKNNIRIADFGWASLQVGSLLLETSCGSPHY	180
Qy	181	ACPEVIKGEYDGRADMWSCGVILFALLVGALPFDNNLRQLLEKVKRGVFMHPHFIPP	240
Db	181	ACPEVIKGEYDGRADMWSCGVILFALLVGALPFDNNLRQLLEKVKRGVFMHPHFIPP	240
Qy	241	DCQSLRLGMLTEVEPEKRLSLEQIKHPWYLGKHEPDCLEPAPGRVAMRSLPSNGELD	300
Db	241	DCQSLRLGMLTEVEPEKRLSLEQIKHPWYLGKHEPDCLEPAPGRVAMRSLPSNGELD	300
Qy	301	PDVLESWASLGCPRDRRLHRELRLSENEQKMIYYILLDRKERYPSCEDQLPDRNDVD	360
Db	301	PDVLESWASLGCPRDRRLHRELRLSENEQKMIYYILLDRKERYPSCEDQLPDRNDVD	360

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QY 361 PPRKRVDSPLSRHGKRRPERKSMVLSITDAGGGSPVTRRALEMAQHSQSRVSQA 420
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|
Db 361 PPRKRVDSPLSRHGKRRPERKSMVLSITDAGGGSPVTRRALEMAQHSQSRVSQA 420
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|
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QY 421 STGLSSPLSSPRSPVFSFPEPCAGDEARGGSPSTKTQLPSRGRGGGAGEQPPPS 480
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Db 421 STGLSSPLSSPRSPVFSFPEPCAGDEARGGSPSTKTQLPSRGRGGGAGEQPPPS 480
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QY 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTPTTTPPPGGVGGAAWRSRLNSI 540
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Db 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTPTTTPPPGGVGGAAWRSRLNSI 540
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|
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QY 541 RNSFLGSPRHRKMQVPTAEEMSSLTPESSPELAKRSWFCNFIISLDKEQIFLVLDKP 600
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Db 541 RNSFLGSPRHRKMQVPTAEEMSSLTPESSPELAKRSWFCNFIISLDKEQIFLVLDKP 600
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QY 601 LSSIKADIVHAFISPLSHSVLSQTSFRAEYKASGSPSVFKPVRFOVDISSSEGEPS 660
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Db 601 LSSIKADIVHAFISPLSHSVLSQTSFRAEYKASGSPSVFKPVRFOVDISSSEGEPS 660
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|
QY 661 PRDGGGGGIYSVTFTLISGPRRRFKRVVETIQAOQLLSTHDSVQALADEKNGAQTRP 720
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Db 661 PRDGGGGGIYSVTFTLISGPRRRFKRVVETIQAOQLLSTHDSVQALADEKNGAQTRP 720
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QY 721 AGAPRSLQPPGRDPELSSSPRRGPKDKKLLATNGTLP 762
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Db 721 AGAPRSLQPPGRDPELSSSPRRGPKDKKLLATNGTLP 762
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RESULT 2
US-10-116-326-6
; Sequence 6, Application US/10116326
; Patent No. 6777545
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6777545el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 703
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-116-326-6

Query Match 87.4%; Score 3545; DB 4; Length 703;
Best Local Similarity 99.7%; Pred. No. 1.7e-231; Indels 0; Gaps 0;
Matches 672; Conservative 1; Mismatches 1;

QY 89 FRYLVLEHVS GGELFDYLVKKGRITPKARKFFRQIVSALDFCHSYISICHRLDKPENLLL 148
|
|
|
Db 30 YLYLVLEHVS GGELFDYLVKKGRITPKARKFFRQIVSALDFCHSYISICHRLDKPENLLL 89
|
|
|
QY 149 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIGKEKYGDRADWMSGCVILFAL 208
|
|
|
Db 90 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIGKEKYGDRADWMSGCVILFAL 149
|
|
|
QY 209 LVGALPDDNNLRLLLEKVKRGVFMHPHFTPPDCQSLLRGWIEVEPEKRLSLEQIQHPW 268
|
|
|
Db 150 LVGALPDDNNLRLLLEKVKRGVFMHPHFTPPDCQSLLRGWIEVEPEKRLSLEQIQHPW 209
|
|
|
QY 269 YLGKKEHPDPCLEPAGRRVAMRSLPSNGELDPDVLESMAISLGCFRDRRLHRLRESEEE 328
|
|
|
Db 210 YLGKKEHPDPCLEPAGRRVAMRSLPSNGELDPDVLESMAISLGCFRDRRLHRLRESEEE 269
|
|
|
QY 329 NOEKMIYLLDRKERYPSCEDQDLPVRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 388
|
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Db 270 NOEKMIYLLDRKERYPSCEDQDLPVRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 329
|
|
|
QY 389 ITDAGGGSPVTRRALEMAQHSQSRVSQTSGLSSPLSSPRSPVFSFPEPCAGDE 448
|
|
|
Db 330 ITDAGGGSPVTRRALEMAQHSQSRVSQTSGLSSPLSSPRSPVFSFPEPCAGDE 389
|
|
|
QY 449 ARGGGSPSTKTQLPSRGRGGGAGEQPPPGARSTPLPGPGSPRSSGGTPLHSPHT 508
|
|
|
Db 390 ARGGGSPSTKTQLPSRGRGGGAGEQPPPGARSTPLPGPGSPRSSGGTPLHSPHT 449
|
|
|
QY 509 RASPTGTPTTTPPPSGGVGGAAWRSRLNSIRNSFLGSPRHRKMQVPTAEEMSSLT 568
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Db 450 RASPTGTPTTTPPPSGGVGGAAWRSRLNSIRNSFLGSPRHRKMQVPTAEEMSSLT 509
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QY 569 ESSPELAKRSWFCNFIISLDKEQIFLVLDKDKPLSSIKADIVHAFISPLSHSVLSQTSF 628
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Db 510 ESSPELAKRSWFCNFIISLDKEQIFLVLDKDKPLSSIKADIVHAFISPLSHSVLSQTSF 569
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|
QY 629 RAEYKASGSPSVFKPVRFOVDISSSEGEPEPRRDGSGGGGIYSVTFTLISGPRRRFKR 688
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|
|
Db 570 RAEYKASGSPSVFKPVRFOVDISSSEGEPEPRRDGSGGGGIYSVTFTLISGPRRRFKR 629
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|
|
QY 689 VVETIQAOQLLSTHDSVQALADEKNGAQTRPAGAPRSLQPPGRDPELSSSPRRGPP 748
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|
|
Db 630 VVETIQAOQLLSTHDSVQALADEKNGAQTRPAGAPRSLQPPGRDPELSSSPRRGPP 689
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|
QY 749 KKKLLATNGTLP 762
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Db 690 KKKLLATNGTLP 703
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RESULT 3
US-10-116-326-2
; Sequence 2, Application US/10116326
; Patent No. 6777545
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6777545el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 778
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-116-326-2

Query Match 87.4%; Score 3545; DB 4; Length 778;
Best Local Similarity 99.7%; Pred. No. 2e-231; Indels 0; Gaps 0;
Matches 672; Conservative 1; Mismatches 1;

QY 89 FRYLVLEHVS GGELFDYLVKKGRITPKARKFFRQIVSALDFCHSYISICHRLDKPENLLL 148
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Db 105 YLYLVLEHVS GGELFDYLVKKGRITPKARKFFRQIVSALDFCHSYISICHRLDKPENLLL 164
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QY 149 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIGKEKYGDRADWMSGCVILFAL 208
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|
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Db 165 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIGKEKYGDRADWMSGCVILFAL 224
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QY 209 LVGALPDDNNLRLLLEKVKRGVFMHPHFTPPDCQSLLRGWIEVEPEKRLSLEQIQHPW 268
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|
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Db 225 LVGALPDDNNLRLLLEKVKRGVFMHPHFTPPDCQSLLRGWIEVEPEKRLSLEQIQHPW 284
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QY 269 YLGKKEHPDPCLEPAGRRVAMRSLPSNGELDPDVLESMAISLGCFRDRRLHRLRESEEE 328
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|
|
Db 285 YLGKKEHPDPCLEPAGRRVAMRSLPSNGELDPDVLESMAISLGCFRDRRLHRLRESEEE 344
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Qy 329 NOEKMIYLLLDKERYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 388
Db 345 NOEKMIYLLLDKERYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 404
Qy 389 ITDAGGGGSPVPTRRALMAQHSQSRSSVSGASTGLSSPLSSPRSPVFSPEPGAGDE 448
Db 405 ITDAGGGGSPVPTRRALMAQHSQSRSSVSGASTGLSSPLSSPRSPVFSPEPGAGDE 464
Qy 449 ARGGGSPSTKTQTLPSRGRGGGAGEQPPPSARSTPLPGPPGSPRSSGGTPLHSLHTP 508
Db 465 ARGGGSPSTKTQTLPSRGRGGGAGEQPPPSARSTPLPGPPGSPRSSGGTPLHSLHTP 524
Qy 509 RASPTGTPGTTPPSPGCGVGGAAWRSLRSLRNSFLGSRPRHRRKMQVPTAEMSSLTP 568
Db 525 RASPTGTPGTTPPSPGCGVGGAAWRSLRSLRNSFLGSRPRHRRKMQVPTAEMSSLTP 584
Qy 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628
Db 585 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644
Qy 629 RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGIYSVTFTLISGSPRRFKR 688
Db 645 RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGIYSVTFTLISGSPRRFKR 704
Qy 689 VVETIOALLSTHDQPSVQALADEKNGAQTREPAGAPRSLOPPGPRDPELSSSPRGPP 748
Db 705 VVETIOALLSTHDQPSVQALADEKNGAQTREPAGAPRSLOPPGPRDPELSSSPRGPP 764
Qy 749 KDKKLLATNGTPLP 762
Db 765 KDKKLLATNGTPLP 778

RESULT 4

US-10-003-690-2
; Sequence 2, Application US/10003690
; Patent No. 6787345
; GENERAL INFORMATION:
; APPLICANT: RORY A.J. CURTIS
; TITLE OF INVENTION: 55053, A No. 6787345el Human Eukaryotic Kinase
; TITLE OF INVENTION: And Uses Therefor
; FILE REFERENCE: WNI-206
; CURRENT APPLICATION NUMBER: US/10/003,690
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/248,893
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 778
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-690-2

Query Match 87.4%; Score 3545; DB 4; Length 778;
Best Local Similarity 99.7%; Pred. No. 2e-231;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 89 FRYLVLEHVS GGELFDYLVKKGRLLTPKEARFFRQIVSALDFCHSYISICHRLDKPENLLL 148
Db 105 YLYLVLEHVS GGELFDYLVKKGRLLTPKEARFFRQIVSALDFCHSYISICHRLDKPENLLL 164
Qy 149 DEKNIRIADFGMASLQVDSLSLETSCGSPHYACPEVIKGEYDGRADMMSCGVILFAL 208
Db 165 DEKNIRIADFGMASLQVDSLSLETSCGSPHYACPEVIKGEYDGRADMMSCGVILFAL 224
Qy 209 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCSSLRGMIEVEPEKRLSLEIQKHPW 268
Db 225 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCSSLRGMIEVEPEKRLSLEIQKHPW 284
Qy 269 YLGKHEPDDCLPAPGRRRVAMRSLPSNGELDDPDVLESMAISLGCFRDRRLHRLRSEEE 328
Db 285 YLGKHEPDDCLPAPGRRRVAMRSLPSNGELDDPDVLESMAISLGCFRDRRLHRLRSEEE 344

Qy 329 NOEKMIYLLLDKERYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 388
Db 345 NOEKMIYLLLDKERYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 404
Qy 389 ITDAGGGGSPVPTRRALMAQHSQSRSSVSGASTGLSSPLSSPRSPVFSPEPGAGDE 448
Db 405 ITDAGGGGSPVPTRRALMAQHSQSRSSVSGASTGLSSPLSSPRSPVFSPEPGAGDE 464
Qy 449 ARGGGSPSTKTQTLPSRGRGGGAGEQPPPSARSTPLPGPPGSPRSSGGTPLHSLHTP 508
Db 465 ARGGGSPSTKTQTLPSRGRGGGAGEQPPPSARSTPLPGPPGSPRSSGGTPLHSLHTP 524
Qy 509 RASPTGTPGTTPPSPGCGVGGAAWRSLRSLRNSFLGSRPRHRRKMQVPTAEMSSLTP 568
Db 525 RASPTGTPGTTPPSPGCGVGGAAWRSLRSLRNSFLGSRPRHRRKMQVPTAEMSSLTP 584
Qy 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628
Db 585 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644
Qy 629 RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGIYSVTFTLISGSPRRFKR 688
Db 645 RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGIYSVTFTLISGSPRRFKR 704
Qy 689 VVETIOALLSTHDQPSVQALADEKNGAQTREPAGAPRSLOPPGPRDPELSSSPRGPP 748
Db 705 VVETIOALLSTHDQPSVQALADEKNGAQTREPAGAPRSLOPPGPRDPELSSSPRGPP 764
Qy 749 KDKKLLATNGTPLP 762
Db 765 KDKKLLATNGTPLP 778

RESULT 5

US-09-930-181-4
; Sequence 4, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-181-4

Query Match 58.9%; Score 2390.5; DB 4; Length 585;
Best Local Similarity 74.4%; Pred. No. 1.4e-153;
Matches 465; Conservative 51; Mismatches 44; Indels 65; Gaps 7;

Qy 90 RYLVLEHVS GGELFDYLVKKGRLLTPKEARFFRQIVSALDFCHSYISICHRLDKPENLLL 149
Db 8 RYLVLEHVS GGELFDYLVKKGRLLTPKEARFFRQIVSALDFCHSYISICHRLDKPENLLL 67
Qy 150 EKNIRIADFGMASLQVDSLSLETSCGSPHYACPEVIKGEYDGRADMMSCGVILFAL 209
Db 68 EKNIRIADFGMASLQVDSLSLETSCGSPHYACPEVIKGEYDGRADMMSCGVILFAL 127
Qy 210 VGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCSSLRGMIEVEPEKRLSLEIQKHPW 269
Db 128 VGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCSSLRGMIEVEPEKRLSLEIQKHPW 187
Qy 270 LGKHEPDDCLPAPGRRRVAMRSLPSNGELDDPDVLESMAISLGCFRDRRLHRLRSEEN 329
Db 188 IGGKNEPEP-EQIP-RKVIRSLPSLEDDPDVLSMHSLSGCFDRDKLLQDLSSEEN 245
Qy 330 QEKMIYLLLDKERYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLSI 389

Db	246	QEKMIYFLLLDRKERYPSEDEBLPRNBIIDPRKRVDSPMLNRHGKRPKRKSMVLSV	305
Qy	390	TDAGCGGSPVPTRRALALEMAHQGRSRVSAGASTGLSSPLSPSPRVFVSFPEPGAGDEA	449
Db	306	TD---GGSPVPARRATEMAHQGRSRISGASGLSTSPSSPR-----	346
Qy	450	RGGSPTSKTQTULPSRGPRGGAGGEPPEPSARSTPLCPGPPSPRSSGGTPLHSPLHTPR	509
Db	347	-----VTPHPSRGSFLPTPKG-----TPVHTPK	370
Qy	510	ASPTGTPGTTPPSPGGGVGGAWRSLRINSIFLGSPRFHRRKMQVPTAEMSLLTPE	569
Db	371	ESFAGTNPPTPSP--SVGGVPMRRLNSIKNSIFLGSPRFHRRKLQVPTPEMSNLTPE	428
Qy	570	SSPELAKRSWFGNFIISLDKEEQIFVLKOKPLSSI KADIVHAFSLTSPISHSVLSQTSFR	629
Db	429	SSPELAKRSWFGNFIISLEKEEQIFVWKOKPLSSI KADIVHAFSLTSPISHSVISQTSFR	488
Qy	630	AEYKASGGSPSVFQKPVRFQVDISSESSEPEPSRRDGGSGGGGIYSVTFTLISGSPSRFKV	689
Db	489	AEYKATGGPAVFQKPVKQFQVDIIYTEGGEAQKE-----NGIYSVTFTLLSGSPSRFKV	542
Qy	690	VETIOAQLLSTHDQPSVOALADEKN	714
Db	543	VETIOAQLLSTHDPPAAACHLSDTTN	567
Qy			

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RESULT 6
US-09-930-181-2
; Sequence 2, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930.181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-181-2

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Query Match	58.8%	Score	2386.5	DB 4	Length	668
Best Local Similarity	74.1%	Pred. No.	3.2e-153	Indels	65	Gaps
Matches	464	Conservative	52	Mismatches	45	
QY	89	FRYLVEHVS	GELFDYLVKKGRLTPKEARKF	FRQIVSALDFCHSYIS	CHRDLPENLLL	148
Db	:					:
QY	90	YLYLVEHVS	GELFDYLVKKGRLTPKEARKF	FRQIISALDFCHSHS	ICHRDLPENLLL	149
Db	:					:
QY	149	DEKNNIRI	ADFQWASIQVGDSLLETSCGSPHYAC	PEVIGKEKYDGRADM	SCGVILFAL	208
Db	:					:
QY	150	DEKNNIRI	ADFQWASIQVGDSLLETSCGSPHYAC	PEVIRGEKYDGRKAD	VWSCGVILFAL	209
Db	:					:
QY	209	LVGALP	PFDDNLRQLLEKVKRGVFHMPHF	IPDDCOSLLRGME	LEVEPEKRLS	EQIQKHPW
Db	:					:
QY	210	LVGALP	PFDDNLRQLLEKVKRGVFHMPHF	IPDDCOSLLRGME	LEVAARLT	LEHLOKHIW
Db	:					:
QY	269	YLGKGHE	PPCLPAPGRVAMRSLPSNGEL	PDFDLVLES	MSAGC	PFDRRLHRELR
Db	:					:
QY	270	YIGGKNE	PEP-EQIP-RKQI	IRSLPSLEDIDPD	VLDMSHSLG	CFDRNKLQDLLS
Db	:					:
QY	329	NQEKMI	YLLLDKERYP	SCEDODLP	RNDVDP	PRKVDSPMLSRHGK
Db	:					:
QY	328	NQEKMI	YFLLLDKERYP	SCEDDL	PERNEIDP	PRKRVDS
Db	:					:
QY	389	ITDAGG	GSVPVTRALEMAQH	QRGRSV	GASTGLSS	PLSPRS
Db	:					:
QY	388	VTD---	GGSPVARRALEMAQH	QRGRSV	ISGASGL	STSPFLSP
Db	:					:

449	ARGGGSP	TSKTQ	TLPSR	GGAG	QPP	PSAR	STPL	PGPP	SGSR	SGGT	PLH	SP	HTP	508
430														
509	RASPTG	TGTT	PPSP	GGV	GGA	NR	SLNS	IRNS	FLGS	PRFR	HR	KMQ	VPTA	EE
453	KESPA	GT	PNPT	PPSS	-	SV	GG	VP	WR	AR	LN	SN	KS	FL
569	ESSPE	LAK	SW	FG	NF	IS	LD	KE	QIF	LV	LK	D	KPL	SS
511	ESSPE	LAK	SW	FG	NF	IS	LD	KE	QIF	LV	LK	D	KPL	SS
629	RASYK	ASG	PS	VP	KV	QR	VD	IS	SE	GE	PE	PR	DR	GS
571	RAEYK	ATG	GP	AV	FQ	KV	KF	QV	DI	TY	TE	GE	AK	QE
689	VVETI	QA	QL	LS	TH	DQ	PS	VQ	AL	DE	KN			
625	VVETI	QA	QL	LS	TH	DQ	PS	VQ	AL	DE	KN			

RESULT 7
 US-09-930-181-17
 ; Sequence 17, Application US/09930181
 ; Patent No. 6455292
 ; GENERAL INFORMATION:
 ; APPLICANT: Origene Technologies
 ; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
 ; FILE REFERENCE: 16U 101 V1
 ; CURRENT APPLICATION NUMBER: US/09/930,181
 ; CURRENT FILING DATE: 2001-08-16
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 17
 ; LENGTH: 603
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-930-181-17

Query Match	58.7%;	Score 2381.5;	DB 4;	Length 603;
Best Local Similarity	71.8%;	Pred. No. 6.1e-153;		
Matches 468;	Conservative 53;	Mismatches 46;	Indels 85;	Gaps 9;
QY	89	FRYLVLHVSGGELFDYLVKKGRITPKEARFFQIIVSALDFCHYSYICHRDLKPENLLL	148	
Db	19	LYLVVLHVSGGELFDYLVKKGRITPKEARFFQIIVSALDFCHSHSICHRDLKPENLLL	78	
QY	149	DEKNNIRIADFGMASIQVDSILLETSCGSPHYACPEVIKGEKYDGRADMMWSCGVILFAL	208	
Db	79	DEKNNIRIADFGMASIQVDSILLETSCGSPHYACPEVIRGEKYDGRKADVWSCGVILFAL	138	
QY	209	LVGALPFDDNLRQLLEKVKGVFHMPIIPDQCOSLLRGMIYEPEKELSLQIQKHPW	268	
Db	139	LVGALPFDDNLRQLLEKVKGVFHMPIIPDQCOSLLRGSEVDAARLTLEHITQKHIW	198	
QY	269	YLGKHEPDPCELPAPGRVRVMSLPSNGELDPDVLSEMASLGCPRDRRLHRELRSEEE	328	
Db	199	YLGKKEPEP-EQPIP-RKVQIRSLPSLEDIPDVLDSMHSILGCPRDRNKLLQDLSSEE	256	
QY	329	NOEKMIYLLLRKERYSPCEODLPPRNDVDPKPKRVDSPLMRHGKRRPERKSMEVLS	388	
Db	257	NOEKMIYFLLLRKERYSQEDEDLPNRNEIDPPKRRVDSPLMNRHGKRRPERKSMEVLS	316	
QY	389	ITDAGGGGSPVTRRALEMAHQSRSRVSGASTGLSSPLSSPRSPVPSFSPGACGDE	448	
Db	317	VTD--GGSPVPARRAIEMAHQGRSRISGASSGLSTSPSSPR-----	358	
QY	449	ARGCGSPTKTQTLPSRGRGGGAGQPPPPARSTPLPGPPGSPRSSGGTPLHGSLHPT	508	
Db	359	-----VTHPSPRGSPLETPKG-----TVHPTP	381	
QY	509	RASPTGTPTPTPPSPGGVGGAWRSLNSTNSFLGSPFRHRRKQKVPTAEEMSSLTP	568	


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QY 443 PGAGDEARGGSGTSKTQTLPSRGRGGAGEQPPPPSARSTPL--PGPEGPRSSGGTP 500
Db 425 PGL---ERKKTTPSTNSVLSTSTN-----RSRNSPLLERASLGQASIQNGKD 470
QY 501 LHSPLHTPRASPT-----GTPGTT-----PPP 522
Db 471 STAPQRPVAPSAHNISSGGAPDRTPFRGVSSRSTFHAGQLQVRDQQLPYGVTPA 530
QY 523 SPGGVGGAARSLRSLRNSFLGSPFRHRRKQVPTABE--MSSLTP-----568
Db 531 SPGSHSQGR--RGASGSIFFSKF--TSKFVRNLNPEPEKDRVETLRPHVVGSGNDKEKE 586
QY 569 ---ESSPELAKRW-FGNFISLDKEQIFLVLDKPLSSIKADIVHAFISLPSLSHVSLS 624
Db 587 EFREAKPRSLRFTWSMKTTSMEPNEMMRIRKVLNDANSQSELHEKYMLL--CMHGTPG 644
QY 625 QTSFRAEYKASGGPSVFQKPRFQVDISSSEGEPEPDRDGGGGGIYSVTFLLISGPR 684
Db 645 HEDF-----VQWEMEYCK-----LPRLSLNG-----VRPKRISGTSM 676
QY 685 RFKRVVETIOAQL 697
Db 677 AFKNIAASKIANEL 689
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RESULT 10

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US-09-984-890-2
; Sequence 2, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-890-2
```

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Query Match 15.7%; Score 636; DB 4; Length 724;
Best Local Similarity 29.1%; Pred. No. 6.9e-35;
Matches 196; Conservative 94; Mismatches 241; Indels 142; Gaps 24;
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QY 91 YLVLEHVGSGELFDYLVKKGRLLTPKEARKFRQIVSALDFCHSYISICHRDLKPENLLLDE 150
Db 126 YLVMEYASGGEVFDYLVAGHRMKEKARAKFRQVSAVQYCHQKFIHVRDLKAENLLLDA 185
QY 151 KNNIRIADFGMASLQVGSLSLETSCGSHYACPEVKEKIDGRRADWMSGCVILFALLV 210
Db 186 DMNIRIADFGSNEFTFGNKLDTFCGSPPYAAPELFGQKYDGPEDVMSLGVILYTLVS 245
QY 211 GALPDDNNLRQLLEKVKRGVFMHPHFIPPCOSILRGMIIEVEPEKRLSLQIOKHPWYL 270
Db 246 GSLPFDQNLKRLRVRIGRYIRIPFYMTSDCNLLKKFLINFSKRGTLQEIWKDRWN 305
QY 271 GKGHEPD---PCLEPAPGRVAMRSLPSNGELDPDVLSEMASLGCFRDRERLHRLSEE 327
Db 306 VG-HEDELKPYVEPLPDYK-----DPRTELWMSMG--YTREIQDSLVGQR 350
QY 328 ENQEKMIYVLLDRKERYPSCEDQLPPRNDVPPRKRVDSPP--MLSRHGKRPERKSM 385
Db 351 YN-EVMATYLLGLGYKSSLEGGDTITLKPRPSADLTNSSAPSPSHKVQSVSANPKQRRF- 408
QY 386 VLSITDAGGSGVPVTPTRALE---MAQHSQRSRSVSGASTGLSSPLSSPRSPVFSFPE 442
Db 409 -----SDQAGPAIPTSYNSYKKTQSNNAENKRPEDRESGRKAS--STAKVPA---SPL 457
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QY 443 PGAGDEARGGSGTSKTQTLPSRGRGGAGEQPPPPSARSTPL--PGPEGPRSSGGTP 500
Db 458 PGL---ERKKTTPSTNSVLSTSTN-----RSRNSPLLERASLGQASIQNGKD 503
QY 501 LHSPLHTPRASPT-----GTPGTT-----PPP 522
Db 504 STAPQRPVAPSAHNISSGGAPDRTPFRGVSSRSTFHAGQLQVRDQQLPYGVTPA 563
QY 523 SPGGVGGAARSLRSLRNSFLGSPFRHRRKQVPTABE--MSSLTP-----568
Db 564 SPGSHSQGR--RGASGSIFFSKF--TSKFVRNLNPEPEKDRVETLRPHVVGSGNDKEKE 619
QY 569 ---ESSPELAKRW-FGNFISLDKEQIFLVLDKPLSSIKADIVHAFISLPSLSHVSLS 624
Db 620 EFREAKPRSLRFTWSMKTTSMEPNEMMRIRKVLNDANSQSELHEKYMLL--CMHGTPG 677
QY 625 QTSFRAEYKASGGPSVFQKPRFQVDISSSEGEPEPDRDGGGGGIYSVTFLLISGPR 684
Db 678 HEDF-----VQWEMEYCK-----LPRLSLNG-----VRPKRISGTSM 709
QY 685 RFKRVVETIOAQL 697
Db 710 AFKNIAASKIANEL 722
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RESULT 11

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US-10-274-194-2
; Sequence 2, Application US/10274194
; Patent No. 6706511
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306DIV
; CURRENT APPLICATION NUMBER: US/10/274,194
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-194-2
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Query Match 15.7%; Score 636; DB 4; Length 724;
Best Local Similarity 29.1%; Pred. No. 6.9e-35;
Matches 196; Conservative 94; Mismatches 241; Indels 142; Gaps 24;
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QY 91 YLVLEHVGSGELFDYLVKKGRLLTPKEARKFRQIVSALDFCHSYISICHRDLKPENLLLDE 150
Db 126 YLVMEYASGGEVFDYLVAGHRMKEKARAKFRQVSAVQYCHQKFIHVRDLKAENLLLDA 185
QY 151 KNNIRIADFGMASLQVGSLSLETSCGSHYACPEVKEKIDGRRADWMSGCVILFALLV 210
Db 186 DMNIRIADFGSNEFTFGNKLDTFCGSPPYAAPELFGQKYDGPEDVMSLGVILYTLVS 245
QY 211 GALPDDNNLRQLLEKVKRGVFMHPHFIPPCOSILRGMIIEVEPEKRLSLQIOKHPWYL 270
Db 246 GSLPFDQNLKRLRVRIGRYIRIPFYMTSDCNLLKKFLINFSKRGTLQEIWKDRWN 305
QY 271 GKGHEPD---PCLEPAPGRVAMRSLPSNGELDPDVLSEMASLGCFRDRERLHRLSEE 327
Db 306 VG-HEDELKPYVEPLPDYK-----DPRTELWMSMG--YTREIQDSLVGQR 350
QY 328 ENQEKMIYVLLDRKERYPSCEDQLPPRNDVPPRKRVDSPP--MLSRHGKRPERKSM 385
Db 351 YN-EVMATYLLGLGYKSSLEGGDTITLKPRPSADLTNSSAPSPSHKVQSVSANPKQRRF- 408
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328	Qy	ENQEKMIYLLLRKERYPSCEQDQLPPRNDVD-----PPRKVD 367
318	Db	YN-EVMATYLLLYGKSELEGDYITILKPRPSADLTNNSAQFPSPHKVQSVSANPKQRRFS 376
368	Qy	S-----PMLSRHGK-----RRPE-----RKSM-----384
377	Db	DQAGPALPITSNSYKKTOSNAENKPEEDRESGRKASSTAKVPASPLPGLERKKTPTP 436
385	Qy	---EVLISITDAGGGGSPVFPTRALEMA--QHSQRSRVSG--ASTGLSSPLSPSPR---433
437	Db	STNSVLSTSTNTRGRNSPLLERASLGOASIQNGKDSLTPMGSRASASTASAAVSAARPROH 496
434	Qy	--SPVFSFSEPCAGDEARGGSPSTKQTLPSSRGP-----RGCGAGSQ---PPP 478
497	Db	QKMSAVHVNKASGLPPTESNCEVPSPPTAPQRPVSPSAINISSGGAPDRTNPPRG 556
479	Qy	PSARSTPLPGPPGSRSSGGTPLHSPHLTPRASGTGTGTPPPSPGGVGGGAWRSLN 538
557	Db	VSSRSTFHAGLRQVRDQONLPY-----GVT-PASPSGHSGQR--RCASG 598
539	Qy	SIRNSFLGSPRPHRRKMOVPAZE-MSSLTP-----ESSPELAKRSH-P 580
599	Db	SIFSKF--TSKFYRRNLNPESKDRVETTLRPHVVGSGNDKEKEEFREAKPRSLRFTWSM 656
581	Qy	GNFISLDKEBQIFLVLKDKPLSSIKADIVHAFSLIPSLSHSVLSQTSFRAEYKASGSPSV 640
657	Db	KTTSSMEPNEMREIRKVLNDANSQSELHEKYMLL--CHGTFCHEDF-----702
641	Qy	FQKVPFRQVDISSEGEPSPRRDGGGGIYSVTFTLISGPRRRFKRVVETTQAOQL 697
703	Db	---VOWEMEVCVK-----LPRLSLNG-----VRFKRISGTSMAFNIAASKIANEL 743

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Db      657 KTTSSMEPNMREIRKVLDAQCSELHEKYMLL--CMAGTGHEDF----- 702
Qy      641 FQKPVRFQVDISSSEGPSPRRDGGSGGGIYSVFTLLISGSPRRFRKRVVETIQAO 697
          |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      703 ----VQWEMEVC-----LPRLSLNG-----VRFRISGTSWAFKNIASKIANEL 743

RESULT 13
US-09-984-890-4
; Sequence 4, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-984-890-4

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Query Match	15.6%;	Score 631;	DB 4;	Length 722;
Best Local Similarity	30.1%;	Pred. No. 1.5e-34;		
Matches 203;	Conservative	90;	Mismatches 235;	Indels 146; Gaps 25;
Qy	91	YLVLEHVSGGELFDYLVKKGRLTPKEARKEFRQIVSALDFCHSYSICHRLDKPENLLLLDE	150	
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Qy	151	KNNIRIADFGMASLQVDSILLETSCGSPHYACBEVYKGEKVDGERADWMSGCVILFALLV	210	
Db	186	DMNIKIADFGSNEFTGNKLDITFCGSPPPYAAAPELFGKKYDGEVDVWSLGVILYITLVS	245	
Qy	211	GALPFFDDNLRQLLEKVKRGVFMHPHPIPPDCOSLLRGMIEVPEPEKLSLEQIQKHPWYL	270	
Db	246	GSLPFFDQNLKEURERVLRKGRIPPYMSTDENLLKKFLILNPSKGTGLEIQMKDRWMN	305	
Qy	271	GGKHPPD---PCLEAPARRVAMRSLPSNGELDPDVLESWASLGCFFDRDLRHLRELSE	327	
Db	306	VG-HEDELKPYVEPLDYK-----DPRRTELMVSVMG---YTRSEIQDSLQVQR	350	

QY 328 ENQEKMIYLLDRKERYPCSCDQDLPRLNDVD-----PPRKRVDS 368
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QY 369 -----PMLSRHCK-----RRPERKSMVLSITDAGGGSPVPTTRALEMAQHSQ 412
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QY 413 RSRVSGASTG--LSSSPLSSPRSPVFSFPEPAGDEARGGSPSTKTQTLPSRGP--- 467
Db 460 RKKTPTPTNSVLSLTSTNSRNSPLD---RASLGQASIQNGKDSAPORVPVAPSAH 516
QY 468 ---RGGGAGEQ---PPPPSARSTPLPGPPSPRSSGGTPLHSPHTPRASPTGPTTTP 521
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QY 522 PSPGGVGGAAWRSRLNSIRNSFLGSPFRHRRKMQVPTAEE-MSSLTP----- 568
Db 561 ASPSGHSGQR--RGASGSIFSKF--TSKFVRNRLNEPESKDRVETTLRPHVVGGGTDKEK 616
QY 569 ----ESSPELAKRSW-FGNFISLDKEEQIFLVLDKPLSSIKADIVHAFSLSPSLSHSVL 623
Db 617 EEFREAKPRSLRFTWSMKTTSMEPNEMREIRKVLDSQSELHERYMLL--CVHGTP 674
QY 624 SOTSFRABYKASGSPVQKPRQVDISSESGEPSPRRDGGGGGIYSVFTFLISGSPS 683
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QY 684 RRFRVETIQAOQL 697
Db 707 MAFKNIASKIANEL 720

RESULT 14

US-10-274-194-4
; Sequence 4, Application US/10274194
; Patent No. 6706511
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306DIV
; CURRENT APPLICATION NUMBER: US/10/274,194
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-274-194-4

Query Match 15.6%; Score 631; DB 4; Length 722;
Best Local Similarity 30.1%; Pred. No. 1.5e-34;
Matches 203; Conservative 90; Mismatches 235; Indels 146; Gaps 25;
QY 91 YLVLEHVSGLGELPDYLVKKRLTPKEARKEFRQIVSALDFCHSYKSIHRDLKPELILLDE 150
Db 126 YLVNEVASGGEVFDYLVHAGRMKEKEARFQIVSAVQYCHQKFIVHRDLKAEILLDA 185
QY 151 KNNIRIADFGWASLQVSDSLSTSCGSPHYACPEVINGEKYDGRADMMWSCGVILFALLV 210
Db 186 DMNIIKIDAFGSNEFTGKLDITFCGSPPPYAAPELFGKGYDGPVDVWSLGVILYTLVS 245
QY 211 GALPFDNDNRQLLEKVRGVFMHPHPIPPDCOSLLRGMTEVEPEKRLSEIQKHPWYL 270
Db 246 GSLPFDQNLKELRERVLRGKIRIPFYMTSDCNLLKKFLILNPSKRGTLQIMKDRWN 305
QY 271 GGRHEPD---PCLEPAPGRVAMRSLPSNGELPDVLESWASLGCFFDRRLHRELRSEE 327
Db 306 VG-HEDELKPYVEPLPDYK-----DPRTELMSVWG--YTRIEIQDSLVGQR 350

Query Match 15.5%; Score 629; DB 4; Length 722;
Best Local Similarity 30.1%; Pred. No. 2e-34;

QY 328 ENQEKMIYLLDRKERYPCSCDQDLPRLNDVD-----PPRKRVDS 368
Db 351 YN-EVMATYLLGYKSSLEGGDTITLKPRPSADLTNSAPSPSHKVQSVSANPKQRSS 409
QY 369 -----PMLSRHCK-----RRPERKSMVLSITDAGGGSPVPTTRALEMAQHSQ 412
Db 410 QDAVPAIPTNSYSKKTQSNNAENKRPBETGRKASST-AKVPASPLP-----GLD 459
QY 413 RSRVSGASTG--LSSSPLSSPRSPVFSFPEPAGDEARGGSPSTKTQTLPSRGP--- 467
Db 460 RKKTPTPTNSVLSLTSTNSRNSPLD---RASLGQASIQNGKDSAPORVPVAPSAH 516
QY 468 ---RGGGAGEQ---PPPPSARSTPLPGPPSPRSSGGTPLHSPHTPRASPTGPTTTP 521
Db 517 NISSSGAPORTNPFPGVSSRSSTFHAGQLQRVDRQNLFP-----GVT-P 560
QY 522 PSPGGVGGAAWRSRLNSIRNSFLGSPFRHRRKMQVPTAEE-MSSLTP----- 568
Db 561 ASPSGHSGQR--RGASGSIFSKF--TSKFVRNRLNEPESKDRVETTLRPHVVGGGTDKEK 616
QY 569 ----ESSPELAKRSW-FGNFISLDKEEQIFLVLDKPLSSIKADIVHAFSLSPSLSHSVL 623
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QY 624 SOTSFRABYKASGSPVQKPRQVDISSESGEPSPRRDGGGGGIYSVFTFLISGSPS 683
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QY 684 RRFRVETIQAOQL 697
Db 707 MAFKNIASKIANEL 720

RESULT 15

US-08-817-832B-32
; Sequence 32, Application US/08817832B
; Patent No. 6579691
; GENERAL INFORMATION:
; APPLICANT: MANDELKOW, Eckhard, et al.
; TITLE OF INVENTION: No. 6579691el Protein Kinase (NPK-110)
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,832B
; FILING DATE: 28-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/04258
; FILING DATE: 30-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 7122.5
; FILING DATE: 28-OCT-1994
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-817-832B-32

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Db 126 YLVMEYASGGGVFDYLYVAHGRMKEKARAKRQIVSAVQYCHHKFIIVHRDLKAENLLDA 185
Qy 151 KNNIRIADFGMASIQVGSLLLETSCGSPHYACPEVIGEKYDGRRADWMSGCVILFALLV 210
Db 186 DMNIIADFGFNEFTGNKLDTCGSPPYAAPLFOGKYDGPEDVWSLGVILYTLVS 245
Qy 211 GALPDDNLRQLLEKVRGVFMHPHPIPPDCQSLLRGMIEVEPEKRLSLEQIQKHFWYL 270
Db 246 GSLPFDQNLKELRERVLRGKRIPIFYMTDCENLLKFLILNPSKRGTLQIMKDRWN 305
Qy 271 GKKHEPD---PCLEPAPCRRVAMRSLPSNGELDDVLESMASLCFDRRLHRLRSEE 327
Db 306 VG-HEDDELKPYVEPLPDYK-----DPRRTLMVSMG--YTREEIQDSLVGQR 350
Qy 328 ENQEKMIYVYLLDRKERYPCEDQDLPRNDVD-----PPRKEVDS 368
Db 351 YN-EVMATYLLGLGYKSSLEGGDTITLXPRPSADLTNSAFSPSHKVORSVSANPKQRSS 409
Qy 369 -----PMLSRHGK-----RRPERKSMEVLSITDAGGGGSPVPTRRALEMAQHSQ 412
Db 410 DQAVPAIPTNSYSYKTKQSNNAENKRPETEETGRKASST-AKVPASPLP-----GLD 459
Qy 413 RSRVSGASTG--LSSGPLSPRPVFSFPEPGAGDEARGGSGPTSKTQTLPSRGP--- 467
Db 460 RKKTTPFTSTNSVLSTSTNRSRNSPLLD---RASLGQASIQNGKDXSTAPQRPVVASPSAH 516
Qy 468 ---RGGGAGEQ---PPPPSARSTPLGPPGSPRSSGGTPLHSLHTPRASFTGTPGTPP 521
Db 517 NISSSGAPDRTNPRGVSSKSTFHAGQLRQVRDQQLPF-----GVT-P 560
Qy 522 PSPGGGVGAARSLNSIRNSFLGSPRFHRRKMQVPTAE-MSSLTP----- 568
Db 561 ASPGHSQGR--RGPSGSIKFP--TSKFVRRNLNEPEKDRVETLPHVVVGGGTDKEK 616
Qy 569 -----ESSPELAKRW-FGNFISLDKEQIFLVLDKPLSLIKADIVHAFLSIPSLSHSVL 623
Db 617 EEPREAKPRSLRFTWSMKTTSSMEPNEMREIRKVLDA NSCQSELHERYMLL--CVHGT 674
Qy 624 SQTSPRAEYKASGSPVQKPVRFQVDISSSEGPSPRRDGGGGGIYSVTFLLISGPS 683
Db 675 GHENF-----VQMEMEVCK-----LPRLSLNG-----VRFKRISGTS 706
Qy 684 RRFKRVVETIQAO 697
Db 707 MAFKNIASKIANEL 720
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Search completed: February 17, 2005, 11:04:18

Job time : 51 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 17, 2005, 10:47:38 ; Search time 139 Seconds
(without alignments)
1793.940 Million cell updates/sec

Title: US-10-803-277-4

Perfect score: 4056

Sequence: 1 MGLEFGLEAGGNWSHPLPG.....PRRGPPKXKLLATNGTFLP 762

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4056	100.0	762	14	US-10-116-326-4
2	4056	100.0	762	16	US-10-803-277-4
3	3545	87.4	703	14	US-10-116-326-6
4	3545	87.4	703	16	US-10-803-277-6
5	3545	87.4	778	14	US-10-354-358-92
6	3545	87.4	778	15	US-10-116-326-2
7	3545	87.4	778	15	US-10-423-543-11
8	3545	87.4	778	16	US-10-803-277-2
9	3545	87.4	778	16	US-10-757-262-136
10	3545	87.4	794	15	US-10-311-034-17
11	3362	82.9	754	16	US-10-479-532-1
12	2654	65.4	506	15	US-10-425-114-54189
13	2390.5	58.9	585	14	US-10-195-072-4

14	2390.5	58.9	585	14	US-10-195-071-4	Sequence 4, Appli
15	2387.5	58.9	674	14	US-10-283-247-2	Sequence 2, Appli
16	2387.5	58.9	674	16	US-10-618-941-78	Sequence 78, Appl
17	2386.5	58.8	608	13	US-10-054-579-4	Sequence 4, Appli
18	2386.5	58.8	664	15	US-10-288-798-18	Sequence 18, Appl
19	2386.5	58.8	664	15	US-10-362-892-18	Sequence 18, Appl
20	2386.5	58.8	668	13	US-10-054-579-2	Sequence 2, Appli
21	2386.5	58.8	668	14	US-10-195-072-2	Sequence 2, Appli
22	2386.5	58.8	668	14	US-10-195-071-2	Sequence 2, Appli
23	2381.5	58.7	603	14	US-10-195-072-17	Sequence 17, Appl
24	2381.5	58.7	603	14	US-10-195-071-17	Sequence 17, Appl
25	2381.5	58.7	614	14	US-10-283-247-9	Sequence 9, Appli
26	2381.5	58.7	614	14	US-10-283-247-10	Sequence 10, Appl
27	2381.5	58.7	674	9	US-09-842-582-2	Sequence 2, Appli
28	2381.5	58.7	674	14	US-10-283-247-7	Sequence 7, Appli
29	2381.5	58.7	674	14	US-10-283-247-8	Sequence 8, Appli
30	2366.5	58.3	636	14	US-10-283-247-5	Sequence 5, Appli
31	2366.5	58.3	688	15	US-10-425-114-54467	Sequence 54467, A
32	1043	25.7	204	15	US-10-276-774-2050	Sequence 2050, Ap
33	979	24.1	301	15	US-10-276-774-1422	Sequence 1422, Ap
34	677	16.7	1518	9	US-09-801-368-152	Sequence 152, App
35	677	16.7	1518	15	US-10-369-493-22243	Sequence 22243, A
36	677	16.7	1518	15	US-10-618-581-11	Sequence 11, Appl
37	657	16.2	1462	15	US-10-618-581-15	Sequence 15, Appl
38	648	16.0	1349	15	US-10-618-581-16	Sequence 16, Appl
39	648	16.0	1369	15	US-10-288-798-7	Sequence 7, Appli
40	648	16.0	1369	15	US-10-362-892-7	Sequence 2, Appli
41	643.5	15.9	783	9	US-09-815-915-2	Sequence 9, Appli
42	643.5	15.9	783	9	US-09-823-187-90	Sequence 90, Appl
43	643.5	15.9	783	14	US-10-393-316-2	Sequence 2, Appli
44	643.5	15.9	826	15	US-10-425-114-54182	Sequence 54182, A
45	637	15.7	691	9	US-09-919-585-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-10-116-326-4
; Sequence 4, Application US/10116326
; Publication No. US20030166889A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: No. US20030166889A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; PRIOR FILING DATE: 2002-04-04
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 762
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-116-326-4

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		Gaps	0				
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Db	1	MGLEFGLEAGGNWSHPLPGSDGNWNLFLPGINGNWSLFLPGTHGNWSLFLPRIMGVGL	60				
Qy	61	CHQEPVEVGDEALWSSTCPQPAPSPISFRYLVLVHVSGLFDFLVKKGLTPEAKRF	120				
Db	61	CHQEPVEVGDEALWSSTCPQPAPSPISFRYLVLVHVSGLFDFLVKKGLTPEAKRF	120				
Qy	121	FRQIVSALDFCHYSICHRDLKPKENLLDKNIRIADFGVASIQVSDSLFETSCGSPHY	180				
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Db 181 ACEVILKGEYDGRADMMSCGVLIFALLVGALEPDDNNLRQLLEKVKRGVFMHPIPP 240
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Db 241 DCQSLLRGMIEVEPEKRLSLEQIQKHPWYLGKHEDPDCLEPAPGRVAMRSLPSNGELD 300
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Db 301 PDVLESASLGCCRDRERLHRELRSSEENQEKMIYVLLLDKERYPSCEDQDLPNRDND 360
QY 361 PPRKRVDS PMLSRHGKRRRPERKSMEVLSITDAGGGSPVPTRALEMAQHSQSRVS 420
Db 361 PPRKRVDS PMLSRHGKRRRPERKSMEVLSITDAGGGSPVPTRALEMAQHSQSRVS 420
QY 421 STGLSSPLSSPRSPVFSFPEAGDEARGGSPSTKTQTLPSRPGGGAGGEQPPPPS 480
Db 421 STGLSSPLSSPRSPVFSFPEAGDEARGGSPSTKTQTLPSRPGGGAGGEQPPPPS 480
QY 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTGTTTPPPSPGGVGGAAWRSRLNSI 540
Db 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTGTTTPPPSPGGVGGAAWRSRLNSI 540
QY 541 RNSFLGSPRHRKMOVPTAEEMSSLTPESSPELAKRSWFGNFI SLDKKEQI FLVLKDKP 600
Db 541 RNSFLGSPRHRKMOVPTAEEMSSLTPESSPELAKRSWFGNFI SLDKKEQI FLVLKDKP 600
QY 601 LSSIKADIVHAFISIPSLSHSVLSQTSFRAEYKASGSPSVFQKPVRFQVDISSEGEPS 660
Db 601 LSSIKADIVHAFISIPSLSHSVLSQTSFRAEYKASGSPSVFQKPVRFQVDISSEGEPS 660
QY 661 PRDGGGGGIYSVTFTLISGSPRRFRKRVVETIQALSLTHDQPSVQALADENKGAQTRP 720
Db 661 PRDGGGGGIYSVTFTLISGSPRRFRKRVVETIQALSLTHDQPSVQALADENKGAQTRP 720
QY 721 AGAPPSLQPPGRPDPELSSSPRRGPPKDKLLATNGTLP 762
Db 721 AGAPPSLQPPGRPDPELSSSPRRGPPKDKLLATNGTLP 762

RESULT 2
US-10-803-277-4
; Sequence 4, Application US/10803277
; Publication No. US20040180416A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/803,277
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/10/116,326
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 762
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-803-277-4

Query Match 100.0%; Score 4056; DB 16; Length 762;
Best Local Similarity 100.0%; Pred. No. 1e-203;
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLEFGLGAGNWSHFLPGSDGNWNLFLPGINGNWSLFLPGTHGNWSLFLPRIMGIVL 60
```

```
Db 1 MGLEFGLGAGNWSHFLPGSDGNWNLFLPGINGNWSLFLPGTHGNWSLFLPRIMGIVL 60
QY 61 CHQEPVEVGEALMSWSTCFQPSAPSI SFRYLVLEHVSGGELFDYLVKKGRLLTPKEAR 120
Db 61 CHQEPVEVGEALMSWSTCFQPSAPSI SFRYLVLEHVSGGELFDYLVKKGRLLTPKEAR 120
QY 121 FRQIVSALDFCHSYSTCHRDLPENLLLDKNNIRIADFGMASLQVGDLSLLETSCSPHY 180
Db 121 FRQIVSALDFCHSYSTCHRDLPENLLLDKNNIRIADFGMASLQVGDLSLLETSCSPHY 180
QY 181 ACEVILKGEYDGRADMMSCGVLIFALLVGALEPDDNNLRQLLEKVKRGVFMHPIPP 240
Db 181 ACEVILKGEYDGRADMMSCGVLIFALLVGALEPDDNNLRQLLEKVKRGVFMHPIPP 240
QY 241 DCQSLLRGMIEVEPEKRLSLEQIQKHPWYLGKHEDPDCLEPAPGRVAMRSLPSNGELD 300
Db 241 DCQSLLRGMIEVEPEKRLSLEQIQKHPWYLGKHEDPDCLEPAPGRVAMRSLPSNGELD 300
QY 301 PDVLESASLGCCRDRERLHRELRSSEENQEKMIYVLLLDKERYPSCEDQDLPNRDND 360
Db 301 PDVLESASLGCCRDRERLHRELRSSEENQEKMIYVLLLDKERYPSCEDQDLPNRDND 360
QY 361 PPRKRVDS PMLSRHGKRRRPERKSMEVLSITDAGGGSPVPTRALEMAQHSQSRVS 420
Db 361 PPRKRVDS PMLSRHGKRRRPERKSMEVLSITDAGGGSPVPTRALEMAQHSQSRVS 420
QY 421 STGLSSPLSSPRSPVFSFPEAGDEARGGSPSTKTQTLPSRPGGGAGGEQPPPPS 480
Db 421 STGLSSPLSSPRSPVFSFPEAGDEARGGSPSTKTQTLPSRPGGGAGGEQPPPPS 480
QY 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTGTTTPPPSPGGVGGAAWRSRLNSI 540
Db 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTGTTTPPPSPGGVGGAAWRSRLNSI 540
QY 541 RNSFLGSPRHRKMOVPTAEEMSSLTPESSPELAKRSWFGNFI SLDKKEQI FLVLKDKP 600
Db 541 RNSFLGSPRHRKMOVPTAEEMSSLTPESSPELAKRSWFGNFI SLDKKEQI FLVLKDKP 600
QY 601 LSSIKADIVHAFISIPSLSHSVLSQTSFRAEYKASGSPSVFQKPVRFQVDISSEGEPS 660
Db 601 LSSIKADIVHAFISIPSLSHSVLSQTSFRAEYKASGSPSVFQKPVRFQVDISSEGEPS 660
QY 661 PRDGGGGGIYSVTFTLISGSPRRFRKRVVETIQALSLTHDQPSVQALADENKGAQTRP 720
Db 661 PRDGGGGGIYSVTFTLISGSPRRFRKRVVETIQALSLTHDQPSVQALADENKGAQTRP 720
QY 721 AGAPPSLQPPGRPDPELSSSPRRGPPKDKLLATNGTLP 762
Db 721 AGAPPSLQPPGRPDPELSSSPRRGPPKDKLLATNGTLP 762

RESULT 3
US-10-116-326-6
; Sequence 6, Application US/10116326
; Publication No. US20030166889A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20030166889A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 703
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-116-326-6
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```
Query Match      87.4%; Score 3545; DB 14; Length 703;
Best Local Similarity 99.7%; Pred. No. 4.4e-177;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 89 FRYLVLEHVS GGELFDYLVKKGR LTPKEARKFFRQIVSALDFCHSYICHRLDKPENLLL 148
Db 30 YLYLVLEHVS GGELFDYLVKKGR LTPKEARKFFRQIVSALDFCHSYICHRLDKPENLLL 89

Qy 149 DEKNIRIADFGMASLQVGDLSLETS CGSPHYACPEVIKGEKYDGRADMMSCGVILFAL 208
Db 90 DEKNIRIADFGMASLQVGDLSLETS CGSPHYACPEVIKGEKYDGRADMMSCGVILFAL 149

Qy 209 LVGALPDDDDNLRLQLLEKVRGVFHMHPFI PPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 268
Db 150 LVGALPDDDDNLRLQLLEKVRGVFHMHPFI PPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 209

Qy 269 YLGCKHEPDPCLPEPAGRRVAMRSLPSNGELDPDVLESMA SLGCFRDRERLHRELSEEE 328
Db 210 YLGCKHEPDPCLPEPAGRRVAMRSLPSNGELDPDVLESMA SLGCFRDRERLHRELSEEE 269

Qy 329 NOEKMIYLLLDKRYPSCEDQDLPPRNDVDPKRKRVDS PMLSRHGKRRPERKSMEVLS 388
Db 270 NOEKMIYLLLDKRYPSCEDQDLPPRNDVDPKRKRVDS PMLSRHGKRRPERKSMEVLS 329

Qy 389 ITDAGGGSPVPTRRALEMAHQSORSRVSGASTGLSSPLS PRSPVFSPEPGAGDE 448
Db 330 ITDAGGGSPVPTRRALEMAHQSORSRVSGASTGLSSPLS PRSPVFSPEPGAGDE 389

Qy 449 ARGGGSPSTKTQLTPSRGPRGGAGEQPPPSARSTPLPGPGSPRSGGTPLHSLHTP 508
Db 390 ARGGGSPSTKTQLTPSRGPRGGAGEQPPPSARSTPLPGPGSPRSGGTPLHSLHTP 449

Qy 509 RASPTGTPTPTPPSPGGVGGAAWRSLRNSIRNSFLGSPFRHRRKMQVPTAEEMSSLTP 568
Db 450 RASPTGTPTPTPPSPGGVGGAAWRSLRNSIRNSFLGSPFRHRRKMQVPTAEEMSSLTP 509

Qy 569 ESSPELAKRSWFGNFI SLDKKEQIFLVLDKPLSSI KADIVHAFSLIPSLSHSVLSQTSF 628
Db 510 ESSPELAKRSWFGNFI SLDKKEQIFLVLDKPLSSI KADIVHAFSLIPSLSHSVLSQTSF 569

Qy 629 RAEYKASGGPVFKQPVRFQVDI SSSEGPSPRRDGGGGIYSVFTLISGSPRRPKR 688
Db 570 RAEYKASGGPVFKQPVRFQVDI SSSEGPSPRRDGGGGIYSVFTLISGSPRRPKR 629

Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQT RPAGAPRSLOPPGPRDPPELSSSPRRGPP 748
Db 630 VVETIQALLSTHDQPSVQALADEKNGAQT RPAGAPRSLOPPGPRDPPELSSSPRRGPP 689

Qy 749 KDKKLLATNGTPLP 762
Db 690 KDKKLLATNGTPLP 703

RESULT 4
US-10-803-277-6
; Sequence 6, Application US/10803277
; Publication No. US20040180416A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friddle, Brian
; APPLICANT: Mathur, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/803,277
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/10/116,326
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 703
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-803-277-6

Query Match      87.4%; Score 3545; DB 16; Length 703;
Best Local Similarity 99.7%; Pred. No. 4.4e-177;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 89 FRYLVLEHVS GGELFDYLVKKGR LTPKEARKFFRQIVSALDFCHSYICHRLDKPENLLL 148
Db 30 YLYLVLEHVS GGELFDYLVKKGR LTPKEARKFFRQIVSALDFCHSYICHRLDKPENLLL 89

Qy 149 DEKNIRIADFGMASLQVGDLSLETS CGSPHYACPEVIKGEKYDGRADMMSCGVILFAL 208
Db 90 DEKNIRIADFGMASLQVGDLSLETS CGSPHYACPEVIKGEKYDGRADMMSCGVILFAL 149

Qy 209 LVGALPDDDDNLRLQLLEKVRGVFHMHPFI PPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 268
Db 150 LVGALPDDDDNLRLQLLEKVRGVFHMHPFI PPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 209

Qy 269 YLGCKHEPDPCLPEPAGRRVAMRSLPSNGELDPDVLESMA SLGCFRDRERLHRELSEEE 328
Db 210 YLGCKHEPDPCLPEPAGRRVAMRSLPSNGELDPDVLESMA SLGCFRDRERLHRELSEEE 269

Qy 329 NOEKMIYLLLDKRYPSCEDQDLPPRNDVDPKRKRVDS PMLSRHGKRRPERKSMEVLS 388
Db 270 NOEKMIYLLLDKRYPSCEDQDLPPRNDVDPKRKRVDS PMLSRHGKRRPERKSMEVLS 329

Qy 389 ITDAGGGSPVPTRRALEMAHQSORSRVSGASTGLSSPLS PRSPVFSPEPGAGDE 448
Db 330 ITDAGGGSPVPTRRALEMAHQSORSRVSGASTGLSSPLS PRSPVFSPEPGAGDE 389

Qy 449 ARGGGSPSTKTQLTPSRGPRGGAGEQPPPSARSTPLPGPGSPRSGGTPLHSLHTP 508
Db 390 ARGGGSPSTKTQLTPSRGPRGGAGEQPPPSARSTPLPGPGSPRSGGTPLHSLHTP 449

Qy 509 RASPTGTPTPTPPSPGGVGGAAWRSLRNSIRNSFLGSPFRHRRKMQVPTAEEMSSLTP 568
Db 450 RASPTGTPTPTPPSPGGVGGAAWRSLRNSIRNSFLGSPFRHRRKMQVPTAEEMSSLTP 509

Qy 569 ESSPELAKRSWFGNFI SLDKKEQIFLVLDKPLSSI KADIVHAFSLIPSLSHSVLSQTSF 628
Db 510 ESSPELAKRSWFGNFI SLDKKEQIFLVLDKPLSSI KADIVHAFSLIPSLSHSVLSQTSF 569

Qy 629 RAEYKASGGPVFKQPVRFQVDI SSSEGPSPRRDGGGGIYSVFTLISGSPRRPKR 688
Db 570 RAEYKASGGPVFKQPVRFQVDI SSSEGPSPRRDGGGGIYSVFTLISGSPRRPKR 629

Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQT RPAGAPRSLOPPGPRDPPELSSSPRRGPP 748
Db 630 VVETIQALLSTHDQPSVQALADEKNGAQT RPAGAPRSLOPPGPRDPPELSSSPRRGPP 689

Qy 749 KDKKLLATNGTPLP 762
Db 690 KDKKLLATNGTPLP 703

RESULT 5
US-10-354-358-92
; Sequence 92, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
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; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 32427, 2160,
; TITLE OF INVENTION: 952, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 3011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MPI02-020PIR0NMIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 778
; TYPE: PRT
; ORGANISM: Homo sapiens
; PS-10-354-358-92

```

	Query Match	87.4%;	Score 3545;	DB 14;	Length 778;
	Best Local Similarity	99.7%;	Pred. No. 4.9e-177;		
	Matches 672;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	89	FRYLVLHVSGGELFDYLVKKGRLLTPKEARKFFRQIVSALDFCHSYISICHRDLKPENLLL	148		
Db	105	YLVLVLHVSGGELFDYLVKKGRLLTPKEARKFFRQIVSALDFCHSYISICHRDLKPENLLL	164		
Qy	149	DEKNRIIADFGMASLQVGDLSLLETSCGSPHYACPEVIKGYDGRADMMSCGVILPAL	208		
Db	165	DEKNRIIADFGMASLQVGDLSLLETSCGSPHYACPEVIKGYDGRADMMSCGVILPAL	224		
Qy	209	LVGALPDDDDNLROLLEKVGKGVFHMHPFIIPDQCOSLLRGMI EVEPEKRLSLEIQKHWP	268		
Db	225	LVGALPDDDDNLROLLEKVGKGVFHMHPFIIPDQCOSLLRGMI EVEPEKRLSLEIQKHWP	284		
Qy	269	YLGKHEPDPCLEPAPGRVAVRSLPSNGELDPDVLESMAISLGCPDRDRERLHRELRSEE	328		
Db	285	YLGKHEPDPCLEPAPGRVAVRSLPSNGELDPDVLESMAISLGCPDRDRERLHRELRSEE	344		
Qy	329	NOEKMIYLLLDLRKERYPSCDEODLPPRNDVDPKRKYDPSMLSRHGKRRPERKSMEVLS	388		
Db	345	NOEKMIYLLLDLRKERYPSCDEODLPPRNDVDPKRKYDPSMLSRHGKRRPERKSMEVLS	404		
Qy	389	ITDAGGGSPVPTTRALEMAHQSRSVSGASTGLSSPISPSRSPVFSFPEPGADGE	448		
Db	405	ITDAGGGSPVPTTRALEMAHQSRSVSGASTGLSSPISPSRSPVFSFPEPGADGE	464		
Qy	449	ARGGSPSTKQTLLPSRPRGGGAGEOPPPESARSTPLPGPPGSPRSSGGTPLHSPHLTP	508		
Db	465	ARGGSPSTKQTLLPSRPRGGGAGEOPPPESARSTPLPGPPGSPRSSGGTPLHSPHLTP	524		
Qy	509	RASPTGTCTTPPPSPGGGVGAAWRSLNIRNSFLGSPRHRRMQVPTAEEMSSLTTP	568		
Db	525	RASPTGTCTTPPPSPGGGVGAAWRSLNIRNSFLGSPRHRRMQVPTAEEMSSLTTP	584		

Qy	569	ESSPELAKRWSFGNFISLDKEEQIFVLVKDKPLSSIKADIVHAFLSIPSLSHSVLSQTSF	629	RAYEKASGGPSVFOKPVRFQVDISSESGPEPSPRRDGGSGGGGIYSVTFTLISGPSRRFKR	688
Db	585	ESSPELAKRWSFGNFISLDKEEQIFVLVKDKPLSSIKADIVHAFLSIPSLSHSVLSQTSF	644	RAYEKASGGPSVFOKPVRFQVDISSESGPEPSPRRDGGSGGGGIYSVTFTLISGPSRRFKR	704
Qy	629	RAYEKASGGPSVFOKPVRFQVDISSESGPEPSPRRDGGSGGGGIYSVTFTLISGPSRRFKR	688	RAYEKASGGPSVFOKPVRFQVDISSESGPEPSPRRDGGSGGGGIYSVTFTLISGPSRRFKR	704
Db	645	RAYEKASGGPSVFOKPVRFQVDISSESGPEPSPRRDGGSGGGGIYSVTFTLISGPSRRFKR	704	RAYEKASGGPSVFOKPVRFQVDISSESGPEPSPRRDGGSGGGGIYSVTFTLISGPSRRFKR	720
Qy	689	VVETIQALLSTHDQPSVOALADKNKAQTRPAGAPPRSLQPPGPRDPDELSSSPRGPP	748	VVETIQALLSTHDQPSVOALADKNKAQTRPAGAPPRSLQPPGPRDPDELSSSPRGPP	764
Db	705	VVETIQALLSTHDQPSVOALADKNKAQTRPAGAPPRSLQPPGPRDPDELSSSPRGPP	764	VVETIQALLSTHDQPSVOALADKNKAQTRPAGAPPRSLQPPGPRDPDELSSSPRGPP	780
Qy	749	KOKKLLATNGTLP 762		KOKKLLATNGTLP 762	
Db	765	KOKKLLATNGTLP 778		KOKKLLATNGTLP 778	

```

RESULT 6
US-10-116-326-2
; Sequence 2, Application US/10116326
; Publication No. US20030166889A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20030166889A1el Human Kinases and Polynucleotides
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 778
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-116-326-2

```

Query Match	87.4%	Score	3545;	DB	14;	Length	778;
Beat Local Similarity	99.7%	Pred. No.	4.9e-177;	Indels	0;	Gaps	0;
Matches	672;	Conservative	1;	Mismatches	1;		
Qy	89	FXYLVLEHVS	GGEFLFDYLVKKGRLTPKEARFFRQIVSALDFCHSYSICHRLDKPENLLL	148			
Db	105	YLYLVLEHVS	GGEFLFDYLVKKGRLTPKEARFFRQIVSALDFCHSYSICHRLDKPENLLL	164			
Qy	149	DEKNIRIAD	FGMASLVQDSILLETSCGSPHYACPEVTKGKYDGRADMWSCGVILFAL	208			
Db	165	DEKNIRIAD	FGMASLVQDSILLETSCGSPHYACPEVTKGKYDGRADMWSCGVILFAL	224			
Qy	209	LVGALPFDD	DDLRLQLLEKVKRGVFMHPHFIPDQCSSLRGMIEVEPEKRLSLEIQKHFW	268			
Db	225	LVGALPFDD	DDLRLQLLEKVKRGVFMHPHFIPDQCSSLRGMIEVEPEKRLSLEIQKHFW	284			
Qy	269	YLGKGHEPD	PCLEPAPGRVAMRSIPNSNGELDPDVLKSWASLGCPRDRERLHRELRSSEE	328			
Db	285	YLGKGHEPD	PCLEPAPGRVAMRSIPNSNGELDPDVLKSWASLGCPRDRERLHRELRSSEE	344			
Qy	329	NQEKMIYLL	LDRKERYPSCEDQDLPNRNDVDPKRVDSPLSHGKRRPERKSMEVLS	388			
Db	345	NQEKMIYLL	LDRKERYPSCEDQDLPNRNDVDPKRVDSPLSHGKRRPERKSMEVLS	404			
Qy	389	ITDAGGGS	VPVTRALEMAQHSQRSRVSGASTGLSSSPLSSPSRSPVFSFSPGAGDE	448			
Db	405	ITDAGGGS	VPVTRALEMAQHSQRSRVSGASTGLSSSPLSSPSRSPVFSFSPGAGDE	464			
Qy	449	ARGGGSPT	SKTQTLPSRGRPGGAGEQPPPSARSTPLPGPPGSRSSCGTDLHSLHPTP	508			
Db	465	ARGGGSPT	SKTQTLPSRGRPGGAGEQPPPSARSTPLPGPPGSRSSCGTDLHSLHPTP	524			
Qy	509	RASPTGT	PGTTPPPSPGGVGGAAMRSLNIRNSFLAGSPRPHRRKQVPTAAEMSSLTP	568			

Db 525 RASPTGPTGTTTPPSGGVGAARSRSLRNSIRNSFLSGSPRFRHRKMQVPTAEEMSLTP 584
Qy 569 ESSPELAKRWFNGFNISLDKEEQIFLVLDKPKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628
Db 585 ESSPELAKRWFNGFNISLDKEEQIFLVLDKPKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644
Qy 629 RAEYKASGGSPVQKPVRFQVDISSSGSPSPRSDGSGGGIYSVTFTLISGSPRRFKR 688
Db 645 RAEYKASGGSPVQKPVRFQVDISSSGSPSPRSDGSGGGIYSVTFTLISGSPRRFKR 704
Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPGRDPPELSSSPRRGPP 748
Db 705 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPGRDPPELSSSPRRGPP 764
Qy 749 KDKKLLATNGTPLP 762
Db 765 KDKKLLATNGTPLP 778

RESULT 7
US-10-423-543-11
; Sequence 11, Application US/10423543
; Publication No. US20040058355A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Libermann, Rosana K.
; APPLICANT: Hunter, John J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Chun, Miyoung
; APPLICANT: Williams, Mark J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
; TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638,
; TITLE OF INVENTION: 18610, 33217, 21967, h1983, m1983, 38555 OR 593 MOLECULES
; TITLE OF INVENTION: AND US\$ THEREFOR
; FILE REFERENCE: MPI03-0230NM
; CURRENT APPLICATION NUMBER: US/10/423,543
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 10/278,036
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 09/711,216
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/205,447
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 10/012,055
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/248,325
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 10/003,690
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/248,893
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 10/217,168
; PRIOR FILING DATE: 2002-08-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 778
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-423-543-11

Query Match 87.4%; Score 3545; DB 15; Length 778;
Best Local Similarity 99.7%; Pred. No. 4.9e-177;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 89 FRYLVLEHVSGBGLFDYLVKKGLTTPKEARKFFRQIVSALDFCHSYICHRLDKPENLLL 148
Db :|||||
Qy 105 YLYLVLEHVSGBGLFDYLVKKGLTTPKEARKFFRQIVSALDFCHSYICHRLDKPENLLL 164
Db :|||||
Qy 149 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIKGEKYDGRADMMSCVILPAL 208
Db DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIKGEKYDGRADMMSCVILPAL 224
Qy 209 LVGALPDDNNLRQLLEKVKRGVFMHPHFTIPPCQSLLRGMI EVEPEKRLSLEQIQHPW 268
Db LVGALPDDNNLRQLLEKVKRGVFMHPHFTIPPCQSLLRGMI EVEPEKRLSLEQIQHPW 284
Qy 269 YLGKKEHPDPCLEPAPGRRVAMRSLPSNGELDPDVLESMASTGLCFRDRERLHRELSEEE 328
Db YLGKKEHPDPCLEPAPGRRVAMRSLPSNGELDPDVLESMASTGLCFRDRERLHRELSEEE 344
Qy 329 NOEKMIYYLLLDKRYPPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 388
Db NOEKMIYYLLLDKRYPPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 404
Qy 389 ITDAGGGSPVPTTRALEMAHQSRSSVSGASTGLSSSLSPSRSPVFSFSPGAGDE 448
Db ITDAGGGSPVPTTRALEMAHQSRSSVSGASTGLSSSLSPSRSPVFSFSPGAGDE 464
Qy 449 ARGGGPTSKTQTLPSRGRGGGAGGEOPPPSARSTPLPGPPGSPRSSGGTPLHSLHTP 508
Db ARGGGPTSKTQTLPSRGRGGGAGGEOPPPSARSTPLPGPPGSPRSSGGTPLHSLHTP 524
Qy 509 RASPTGPTGTTTPPSGGVGAARSRSLRNSIRNSFLSGSPRFRHRKMQVPTAEEMSLTP 568
Db RASPTGPTGTTTPPSGGVGAARSRSLRNSIRNSFLSGSPRFRHRKMQVPTAEEMSLTP 584
Qy 569 ESSPELAKRWFNGFNISLDKEEQIFLVLDKPKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628
Db ESSPELAKRWFNGFNISLDKEEQIFLVLDKPKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644
Qy 629 RAEYKASGGSPVQKPVRFQVDISSSGSPSPRSDGSGGGIYSVTFTLISGSPRRFKR 688
Db RAEYKASGGSPVQKPVRFQVDISSSGSPSPRSDGSGGGIYSVTFTLISGSPRRFKR 704
Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPGRDPPELSSSPRRGPP 748
Db VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPGRDPPELSSSPRRGPP 764
Qy 749 KDKKLLATNGTPLP 762
Db 765 KDKKLLATNGTPLP 778

RESULT 8
US-10-803-277-2
; Sequence 2, Application US/10803277
; Publication No. US20040180416A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/803,277
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/10/116,326
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 778

Qy 629 RAEYKASGSPSVFQKPVRFQVDISSSEGPSPRRDGGGGGIYSVFTTILSGSPRRFKR 688
Db 645 RAEYKASGSPSVFQKPVRFQVDISSSEGPSPRRDGGGGGIYSVFTTILSGSPRRFKR 704
Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTTPAGAPPRSLQPPGRDPPELSSSPRRGPP 748
Db 705 VVETIQALLSTHDQPSVQALADEKNGAQTTPAGAPPRSLQPPGRDPPELSSSPRRGPP 764
Qy 749 KDKKLLATNGTPLP 762
Db 765 KDKKLLATNGTPLP 778

RESULT 10
US-10-311-034-17
; Sequence 17, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAPALIA, April
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: LO, Terence P.
; APPLICANT: KHAH, Farrah A.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GREYER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeev
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311.034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 794
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 7477486CD1
US-10-311-034-17

Query Match 87.4%; Score 3545; DB 15; Length 794;
Best Local Similarity 99.7%; Pred. No. 5e-177;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 89 FRYLVLEHVHSGGELFDYLVKKGRLLTPKEARKFFRQIVSALDFCHSYSGICHRDLKPENL 148
Db 121 YLYLVLEHVHSGGELFDYLVKKGRLLTPKEARKFFRQIVSALDFCHSYSGICHRDLKPENL 180
Qy 149 DEKNRIADFGMASLQVGSLLTSCGSPHYACPEVIKGEKYDGRADWMSGVILPAL 208
Db 181 DEKNRIADFGMASLQVGSLLTSCGSPHYACPEVIKGEKYDGRADWMSGVILPAL 240
Qy 209 LVGALPDDDNRLQLLEKVRGVFHPHF1PPDCQSLRLGMI EVEPKRSLSEIOIQHPW 268
Db 241 LVGALPDDDNRLQLLEKVRGVFHPHF1PPDCQSLRLGMI EVEPKRSLSEIOIQHPW 300
Qy 269 YLGGKHEPDPCLPEPAGRRVAMRSLPSNGELDPDVLSEMASLGCFRDRERLHRLSEEE 328
Db 301 YLGGKHEPDPCLPEPAGRRVAMRSLPSNGELDPDVLSEMASLGCFRDRERLHRLSEEE 360
Qy 329 NOEKMIYLLLDKRYPCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 388
Db 361 NOEKMIYLLLDKRYPCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 420
Qy 389 ITDAGGGSPVPTRRALEMAQHSORSVSAGSTGLSSSLSSPSRSPVFSPEPGAGDE 448
Db 421 ITDAGGGSPVPTRRALEMAQHSORSVSAGSTGLSSSLSSPSRSPVFSPEPGAGDE 480
Qy 449 ARGGSPTSQTQLPSRGRGGGAGEOPPPPSARSTPLPGPPSPRSSGGTPLHSLHTP 508
Db 481 ARGGSPTSQTQLPSRGRGGGAGEOPPPPSARSTPLPGPPSPRSSGGTPLHSLHTP 540
Qy 509 RASPTGPTTTPPPSGGVGGAARSLRSLNINSFLGSPRFRHRKQVPTAEEMSSLT 568
Db 541 RASPTGPTTTPPPSGGVGGAARSLRSLNINSFLGSPRFRHRKQVPTAEEMSSLT 600
Qy 569 ESSPELAKRSWFGNFI SLDKKEQIFLVLDKPLSSIKADIVHAPLSIPSLSHSVLSQTSF 628
Db 601 ESSPELAKRSWFGNFI SLDKKEQIFLVLDKPLSSIKADIVHAPLSIPSLSHSVLSQTSF 660
Qy 629 RAEYKASGSPSVFQKPVRFQVDISSSEGPSPRRDGGGGGIYSVFTTILSGSPRRFKR 688
Db 661 RAEYKASGSPSVFQKPVRFQVDISSSEGPSPRRDGGGGGIYSVFTTILSGSPRRFKR 720
Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTTPAGAPPRSLQPPGRDPPELSSSPRRGPP 748
Db 721 VVETIQALLSTHDQPSVQALADEKNGAQTTPAGAPPRSLQPPGRDPPELSSSPRRGPP 780
Qy 749 KDKKLLATNGTPLP 762
Db 781 KDKKLLATNGTPLP 794

RESULT 11
US-10-479-532-1
; Sequence 1, Application US/10479532
; Publication No. US20040151713A1
; GENERAL INFORMATION:
; APPLICANT: TAIHO PHARMACEUTICAL CO., LTD
; TITLE OF INVENTION: CELL CYCLE REGULATORY FACTOR
; FILE REFERENCE: 44B00JP
; CURRENT APPLICATION NUMBER: US/10/479,532
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: JP 2001-168792
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 754
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-479-532-1

Query Match 82.9%; Score 3362; DB 16; Length 754;
Best Local Similarity 95.4%; Pred. No. 1.7e-167; Indels 24; Gaps 1;
Matches 643; Conservative 1; Mismatches 6;
QY 89 FRYLVLEHVS GGLFDYLVKKGRLTPKEARKFPRQIVSALDFCHSYSI CHRDLPENLLL 148
DB 105 YLYLVLEHVS GGLFDYLVKKGRLTPKEARKFPRQIVVCGAGLCHSYSI CHRDLPENLLL 164
QY 149 DEKNIRIADFGMASLQVGSLLTSCGSHYACPEVIKGEKDGDRADWSCGVILFAL 208
DB 165 DEKNIRIADFGMASLQVGSLLTSCGSHYACPEVIKGEKDGDRADWSCGVILFAL 224
QY 209 LVGALPDDDNILQLLEKVRGVFPHFIPDQCQSLLRGMIEVEPEKLSLEQIOKHPW 268
DB 225 LVGALPDDDNILQLLEKVRGVFPHFIPDQCQSLLRGMIEVEPEKLSLEQIOKHPW 284
QY 269 YLGCKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLMSASLCCFRDRERLHRELSEEE 328
DB 285 YLGCKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLMSASLCCFRDRERLHRELSEEE 344
QY 329 NOERMIYLLLDLRKERYPSCEDQDLPDRNDVDPKREKVDSPMLSRHCKRPERKSMVLS 388
DB 345 NOERMIYLLLDLRKERYPSCEDQDLPDRNDVDPKREKVDSPMLSRHCKRPERKSMVLS 404
QY 389 ITDAGGSGSPVPTRRALMAQHSORSVSGASTGLSSPLSSPRSPVFSFPEPGAGDE 448
DB 405 ITDAGGSGSPVPTRRALMAQHSORSVSGASTGLSSPLSSPRSPVFSFPEPGAGDE 464
QY 449 ARGGGSPTSQTQTLPSPRGGGAGEQPPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 508
DB 465 ARGGGSPTSQTQTLPSPRGGGAGEQPPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 500
QY 509 RASPTGPTTTPSPSGGVGGAWRSLNIRNSFLGSPRHRKMOVPTAEEMSLTP 568
DB 501 RASPTGPTTTPSPSGGVGGAWRSLNIRNSFLGSPRHRKMOVPTAEEMSLTP 560
QY 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADI VHAFLSIPSLSHSVLSQTSF 628
DB 561 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADI VHAFLSIPSLSHSVLSQTSF 620
QY 629 RAEYKASGGPSVFOKPVRFQVDIISSEGEPEPSRRDGGGGGIYSVFTLISGSRFRK 688
DB 621 RAEYKASGGPSVFOKPVRFQVDIISSEGEPEPSRRDGGGGGIYSVFTLISGSRFRK 680
QY 689 VVETIQALLSHDQPSVQALADEKNGAQTRPAGAPPSLOPPGPPDPELSSSPRRGPP 748
DB 681 VVETIQALLSHDQPSVQALADEKNGAQTRPAGAPPSLOPPGPPDPELSSSPRRGPP 740
QY 749 KDKLLATNGTPLP 762
DB 741 KDKLLATNGTPLP 754
RESULT 12
US-10-425-114-54189
; Sequence 54189, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54189
; LENGTH: 506
; TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
; OTHER INFORMATION: Clone ID: LTB4653-002-E1_FLI.pep
US-10-425-114-54189
Query Match 65.4%; Score 2654; DB 15; Length 506;
Best Local Similarity 99.8%; Pred. No. 9.9e-131; Indels 0; Gaps 0;
Matches 505; Conservative 0; Mismatches 1;
QY 257 RLSLFOIQKHFWYLGCKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLMSASLCCFRDR 316
DB 1 RUSLEQIQKHFWYLGCKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLMSASLCCFRDR 60
QY 317 ERLHRELSEENQEKMIYLLLDLRKERYPSCEDQDLPDRNDVDPKREKVDSPMLSRHCK 376
DB 61 ERLHRELSEENQEKMIYLLLDLRKERYPSCEDQDLPDRNDVDPKREKVDSPMLSRHCK 120
QY 377 RPERKSMVLSITDAGGSGSPVPTRRALMAQHSORSVSGASTGLSSPLSSPRSPV 436
DB 121 RPERKSMVLSITDAGGSGSPVPTRRALMAQHSORSVSGASTGLSSPLSSPRSPV 180
QY 437 FSPSPGAGDEARGGSGPTSQTQLPSRGRGGAGEQPPPPSARSTPLPGPGSPRSS 496
DB 181 FSPSPGAGDEARGGSGPTSQTQLPSRGRGGAGEQPPPPSARSTPLPGPGSPRSS 240
QY 497 GGTPLHSLHTPRASPTGPTTTPSPSGGVGGAWRSLNIRNSFLGSPRHRKMO 556
DB 241 GGTPLHSLHTPRASPTGPTTTPSPSGGVGGAWRSLNIRNSFLGSPRHRKMO 300
QY 557 VPTAEEMSLTPESPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADI VHAFLSIP 616
DB 301 VPTAEEMSLTPESPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADI VHAFLSIP 360
QY 617 SLSHSVLSQTSFRAEYKASGGPSVFOKPVRFQVDIISSEGEPEPSRRDGGGGGIYSVTF 676
DB 361 SLSHSVLSQTSFRAEYKASGGPSVFOKPVRFQVDIISSEGEPEPSRRDGGGGGIYSVTF 420
QY 677 TLISGSRFRKRVETIQALLSHDQPSVQALADEKNGAQTRPAGAPPSLOPPGPPRDP 736
DB 421 TLISGSRFRKRVETIQALLSHDQPSVQALADEKNGAQTRPAGAPPSLOPPGPPRDP 480
QY 737 PELSSSPRRGPPKDKLLATNGTPLP 762
DB 481 PELSSSPRRGPPKDKLLATNGTPLP 506
RESULT 13
US-10-195-072-4
; Sequence 4, Application US/10195072
; Publication No. US20030092036A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195,072
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-072-4
Query Match 58.9%; Score 2390.5; DB 14; Length 585;
Best Local Similarity 74.4%; Pred. No. 6.5e-117; Indels 65; Gaps 7;
Matches 465; Conservative 51; Mismatches 44;
QY 90 RYLVLHVHSGGELFDYLVKKGRLTPKEARKFPRQIVSALDFCHSYSI CHRDLPENLLLD 149
DB 8 RYLVLHVHSGGELFDYLVKKGRLTPKEARKFPRQIVSALDFCHSYSI CHRDLPENLLLD 67

150	QY	EKNIRIADFGWASIQVGD	SLLETS	SCGSPHYAC	PEVTK	BKGYDGR	ADMMWSC	GVIL	FALL	209																	
68	Db	EKNIRIADFGWASIQVGD	SLLETS	SCGSPHYAC	PEVIR	EKYGDK	ADVMSC	GVIL	FALL	127																	
210	QY	VGALPDDDNLRQLLEK	VKRGVFM	HPHFI	PPDCOS	LLRG	MEVE	PKR	LSLEOIQ	HPY 269																	
128	Db	VGALPDDDNLRQLLEK	VKRGVFM	HPHFI	PPDCOS	LLRG	MEV	DAARR	LFLHEIQ	HYI 187																	
270	QY	LGKGHPDPCLEPAPGR	RVAMRSL	PSNGEL	DPDVL	ESWAS	IGLCF	RDRER	LHRLR	SEEN 329																	
188	Db	IGGKNEPEP-EQIP	P-RKVQ	IRSLPS	LEDIP	DVLD	SMHSL	GCFRD	RNKLQ	DLLEEN 245																	
330	QY	QEKMIYYLLDRKERY	PCSEOD	PLPRND	VDP	PKRV	VDSP	MLSR	HGKR	PERKSM	VL 389																
246	Db	QEKMIYFLLDRKERY	PCSEOD	PLPRNE	IDP	PKRV	VDSP	MLSR	HGKR	PERKSM	VL 305																
390	QY	TIAGGGGSPVTRRALE	WAHQSR	SRSVSG	ASTGL	SSPL	SSPRS	PVFS	SP	PGAD	EA 449																
306	Db	TD---GGSPVARRAIE	WAHQSR	SRSTSG	ASSGL	STSP	LSR	---	---	---	346																
450	QY	RGGSPTSKTQTLPR	SRGPRGG	AGEQ	PPPP	GA	RTPL	FGPP	GP	SRSG	TPLHSL	TPR 509															
347	Db	-----VTPH	SPRCS	PLTP	KG-----	---	---	---	---	---	---	TPVHT	PK 370														
510	QY	ASPTGTGTTTTPPSP	GGGVGA	NRSLN	STRNS	FLG	SPR	HRKQ	QVPT	AE	MS	SLT	PE 569														
371	Db	ESPA	GTNP	NTPP	SSP--	--SVG	GVPM	RRAR	LNSIK	NS	FLG	SPR	HRK	LQ	VPTPE	MS	SLT	PE 428									
570	QY	SSPELAK	SWFNG	FTSL	OK	EQI	FLV	LK	DPL	SSI	KADI	VHAF	LS	TPSL	SHSV	LS	OT	SPR 629									
429	Db	SSPELAK	SWFNG	FTSL	OK	EQI	FWI	LK	DPL	SSI	KADI	VHAF	LS	TPSL	SHSV	LS	OT	SPR 488									
630	QY	ASYKAS	GGSP	SV	PKV	TR	QV	DIS	SE	GP	PE	PR	DG	GG	GG	GG	GG	GG	GG 689								
489	Db	AEYKAT	GGPA	V	Q	PKV	Q	V	I	T	Y	T	E	G	E	A	K	E	-----NGI	SV	TP	TL	LS	GG	SR	FK	V 542
690	QY	VETIO	Q	ALL	ST	H	D	Q	P	S	V	A	L	A	D	E	K	N 714									
543	Db	VETIO	Q	ALL	ST	H	D	P	P	A	A	O	H	L	S	T	T	N 567									

RESULT 14

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RESULT 14
US-10-195-071-4
; Sequence 4, Application US/10195071
; Publication No. US20030096271A1
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C1
; CURRENT APPLICATION NUMBER: US/10/195,071
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-195-071-4

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Qy	210	VGALPDDDNLRQLLEKVKRGVFMHPHFPDPCQCSLLRGWIEVEPEKRLSLEQIQKHPWY	269
Db	128	VGALPDDDNLRQLLEKVKRGVFMHPHFPDPCQCSLLRGWIEVDAARLTLEHIQKHIWY	187
Qy	270	LGCKHPEPDCLEPAQRRRVAMRSLPSNGELDPDVLESMASLGCFCRDRERLHRELRESEEN	329
Db	188	IGGKNEPEP-EQPIP-RKQVIRSLPSLEDDPDVLDMSHSLGCFCRDNKULQOLLSEEN	245
Qy	330	QEKMIYLLLDKREYPSCEBODLPNDVDPPRKVDSPMLSRHGKRRRPERKSMEVLSI	389
Db	246	QEKMIYLLLDKREYPSQEBEDLPNRNEIDPPRKVDSPMLNRHGKRRRPERKSMEVLSV	305
Qy	390	TDAGGGSPVPTRRALEMAQHSQRSSVSGASTGLSSPLSSPRSPVFSPPFGAGDEA	449
Db	306	TD---GGSPVPARRAEMAQHGRSSRSISGASSGLSTSPSSPR-----	346
Qy	450	RGGGSPTSQTUTLPSRGRPGGGAGEGPPPPSARSTPLPGPPGSPRSGGTPLHSLHTPR	509
Db	347	-----VTPHSPRSGPLTPKG-----TPVHTPK	370
Qy	510	ASPTGTGTPPPSPGGYGGAARSLKNSIRNSFLGSPRFRHRKMOVPTAEBSMSLTPE	569
Db	371	ESPAGTNPPTPPSSP--SVGGVPMWARLNSIKNSFLGSPRFRHRKQVPTPEMSNLTPE	428
Qy	570	SSPELAKRSMFGNFISLDKEEQIFVLVKDKPLSSIKADIIVHAFSLSPSLSHSVLSQTSFR	629
Db	429	SSPELAKRSMFGNFISLEKEEQIFVVKDKPLSSIADIIVHAFSLSPSLSHSVLSQTSFR	488
Qy	630	AYKASGGPSVFOKPVRFQVDISSSEGBEPSPRRDGGGGGGIVTFTTLISGSPRRFKRV	689
Db	489	AYKATGGPAVFOKPVKFQVDIITYEGGEAQKE-----NGIYSVTFTLLSGSPRRFKRV	542
Qy	690	VETIQALLSTHQPSVQALADEKN	714
Db	543	VETIQALLSTHDPFAAQHLSDTTN	567

RESULT 15

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US-10-283-247-2
; Sequence 2, Application US/10283247
; Publication NO. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-247-2

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[illegible]

89	FRYLVLVLEHVSGBGLFDYLVLKKGRLTLPKEARKFPQIVSALDFCHSVSYICHRLDKPENLLL	Qy
90	YLYLVLEHVSGBGLFDYLVLKKGRLTLPKEARKFPQIIISALDFCHSHSICHRLDKPENLLL	Db
149	DEKNRIADFGMASLQVGDLSILETSCGSHYACPEVIKGEKYDGRADMMWSCGVILFAL	Qy
150	DEKNRIADFGMASLQVGDLSILETSCGSHYACPEVIRGEKYDGRADVMWSCGVILFAL	Db
209	LVGALPDDNDNLRLQLLEKVKRGVFHMPHFIPPOCSLLRGMI EVEPEKRLSLEQIQKHPW	Qy
210	LVGALPDDNDNLRLQLLEKVKRGVFHMPHFIPPOCSLLRGMI EYDAARRLTLSHIOKHIV	Db

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 10:38:35 ; Search time 44 Seconds
(without alignments)
1666.299 Million cell upd

Title: US-10-803-277-4
 Perfect score: 4056
 Sequence: 1 MGLEGFLEAGGNWSHFLEPG.....PRRGPPKDKKLLATNGTPLP 762

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1: *

```
2: pir2:*
```

```
3: pir3: *
4: pir4: *
```

4: p174:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1383	34.1	887	2	T20941	hypothetical prote
2	677	16.7	1518	2	S37928	probable purine nu
3	637	15.7	745	2	G01025	serine/threonine p
4	624	15.4	512	1	JC1446	serine/threonine-s
5	623.5	15.4	775	2	T38929	changed division r
6	618	15.2	504	2	T10449	probable serine/th
7	616	15.2	1192	2	T18611	probable serine/th
8	608	15.0	713	2	S27966	probable serine/th
9	604	14.9	1142	2	S59359	GIN4 protein - yea
10	599	14.8	512	2	T07788	probable serine/th
11	598	14.7	1246	2	G85287	protein H39H23.1 [
12	597	14.7	774	2	I48609	probable serine/th
13	595	14.7	504	2	T07415	probable serine/th
14	595	14.7	562	2	T29858	hypothetical prote
15	594.5	14.7	473	1	S59941	serine/threonine-s
16	593	14.6	401	2	B90120	SNF1-related prote
17	593	14.6	511	1	A56009	serine/threonine-s
18	592	14.6	512	2	T52633	serine/threonine-s
19	588	14.5	798	2	JC7500	serine/threonine-s
20	573.5	14.1	1398	2	T13741	gik hypothetical ch
21	568.5	14.0	513	1	S60303	hypothetical prote
22	566	14.0	576	2	T41587	serine/threonine-s
23	564	13.9	915	2	S74283	probable carbon ca
24	563	13.9	726	2	T33998	probable protein k
25	556.5	13.7	513	1	S60304	hypothetical prote
26	545.5	13.4	552	1	S51025	serine/threonine-s
27	545.5	13.4	891	2	T40503	protein kinase glt
28	545	13.4	502	1	A41361	serine/threonine-s
29	542.5	13.4	552	1	A53621	[hydroxymethylglut

ALIGNMENTS

RESULT 1

T20941

hypothetical protein F15A2.6 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T20941

R;Gregory, J.

submitted to the EMBL Data Library, March 1996

A;Reference number: Z19349

A;Accession: T20941

A; Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-887 <WIL>

A; Cross-references: UNIPROT:Q19469

A; Experimental source: clone F15A2
C: Genetics.

C;Genetics:
A:Gene: CFSP.F15A3 6

A;Gene: CESP:F15A
A:Map position: x

A;Map position: X

Query Match	34.1%	Score 1383;	DB 2;	Length 887;
Best Local Similarity	46.5%;	Pred. No. 1.3e-41;		
Matches	322;	Conservative 84;	Mismatches 191;	Indels 96; Gaps 18;
Qy	89	FRYLVLVHVS	GGGEFLDYLVKKGLRTPKEAKRFQIVSALDFCHSYISICHRDLKAPENLLL	148
Db	91	LYLVLLVHVS	GGGEFLDYLVKRGRLMSKEAKRFQIIISALDFCHAHNIICHRDLKAPENLLL	150
Qy	149	DEKNRIADFGMAS	LQVGSLSLETSCGSPHYACPEVIKGEYDGRADRMWSCGVILFAL	208
Db	151	DERNNIKVADFGMAS	LQVEGSMLETSCGSPHYACPEVIRGEYDGRKADVMSCGVILVAL	210
Qy	209	LVGALPDDDNIL	QQLLEKVRGVFHPHPFPPDCQSLLRGMI EVEPEKRLSLEQIQKHPW	268
Db	211	LVGALPDDDNIL	NLLEKVRGVFHPFHPFVPADVQSLLRAMI EVDPKRYSLADVFKHPW	270
Qy	269	YLGKXHPDPCL	EPAPGRRVAMRSLPSNGSLDPDVLMSASLGCFRDRERLHRLRSEEE	328
Db	271	-VSGTTKAD	PELELPMSQVVQTHVIPGEDSIDPDVLEHMNCLGCFKDKQKLINELLSPKH	329
Qy	329	NQKMYIYLLLD	RKERYPSCEDQ-DLPPR---NDVDPKRKVDSPLMRHGKRRPERSKM	384
Db	330	NTEKMYVYLLD	RKRRAQAQEDTEIVLRGAQAQNNDPKRTDSRSTRY-----	379
Qy	385	EVLISITDAG	GGGSPVPTRRALAMQAHSQRKSYSVGASTGLSSPSLSPSPSPV-----	F 437
Db	380	PMGSIAD-----	GGFIPNPKTYIGRNQKSGRHSILGG-----SPTESPRSTRDLFGSSS	428
Qy	438	SFSPPEGAG	DEARGGGSPTSKT-----QTLPS-----RGPREGGAGE	474
Db	429	SGSVYARAG	DRGRSASRSTNSYHYITVPDPQTLEAAHRVDRQAERRESRDSGRGS	488

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QY 475 -----QPPPSARSTPLPGPPGSRSSGGTPLHSLPHTPRASPTGTP 516
Db 489 SRKESKDRSDKSSASSCKNDASSTSVPHKYSPSPVMSSESVVSSWTNNTSSNSLI 548
QY 517 GTTPPPSGGSGGAWSRLNRSFLGSPFRHRRKQVPTAEEMSSLTPE-SSPELA 575
Db 549 AGNSQTSIGSTSG--PWRSKLNNIKNSFLGTPFRHRRKMSNGTAESDSDSQMIDTDLV 606
QY 576 KRSWFGNF---ISLDKEEQFLVLKOKPLSSIADIVHAFSLSPSLSHSVLSQTSFRAEY 632
Db 607 KKSWMFGSLASSMVERDDTHCVFQGGKTLNSIKAEILRAFLQIHELHSHSVVGGQNCFRVEY 666
QY 633 K--ASGGPSVFQKPVRFQVVISSESGPEPRRDG-SGGGGIYVTFTLISGFSRRFRKV 689
Db 667 KRGPVGGSVFSGIKMNVII-----PSPQQVVIAGETPTVVQFVLLAGPVRRFKRL 720
QY 690 VETIQALLSHDPOPSVOALADEKNGA--QTRP 720
Db 721 VEHLISAIL-----QNSTQQRADROQAALMVRP 748

RESULT 2
S37928
probable purine nucleotide-binding protein YKL101w - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YKL453
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Aug-2004
C;Accession: S37928; S39084
R;Cheret, G.; Fukuhara, H.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Pallier, C.; Puzos
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37928
A;Accession: S37928
A;Molecule type: DNA
A;Residues: 1-1518 <CHR>
A;Cross-references: UNIPROT:P34244; EMBL:Z28101; NID:9486168; PIDN:CAA81941.1; PID:94861
A;Experimental source: strain S288C
R;Pallier, C.; Valens, M.; Puzos, V.; Fukuhara, H.; Cheret, G.; Sor, F.; Bolotin-Fukuhara
Yeast 9, 1149-1155, 1993
A;Title: DNA sequence analysis of a 17 kb fragment of yeast chromosome XI physically loc
protein kinases.
A;Reference number: S39084; MUID:94078677; PMID:8256524
A;Accession: S39084
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-1518 <PAL>
A;Cross-references: EMBL:X71133; NID:9431205; PIDN:CAA50456.1; PID:9431215
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:HSL1
A;Cross-references: SGD:S0001584; MIPS:YKL101w
A;Map position: 11L
C;Superfamily: protein kinase homology
C;Keywords: ATP; P-loop; purine nucleotide binding; serine/threonine-specific protein ki
F;79-369/Domain: protein kinase homology <kin>
F;79-86/Region: nucleotide-binding motif A (P-loop)
F;87-95/Region: protein kinase ATP-binding motif
F;85/Binding site: ATP/GTP (Lys) #status predicted

Query Match 16.7%; Score 677; DB 2; Length 1518;
Best Local Similarity 27.5%; Pred. No. 7.1e-17;
Matches 216; Conservative 120; Mismatches 240; Indels 210; Gaps 27;

QY 91 YLVLEHVS GGELFDYLVKKGRLTPKEARKFRQIVSALDFCHSYISICHRLDKPENLLDE 150
Db 190 YLVLEVDVGGELFDYLVSKGLPEREATHYFKQIVGVSYCHSFNICHRLDKPENLLDK 249
QY 151 KN-NTRIDAFGNASIQVDSGLLETSCGSPHVACPVIKGEYKDGRRADWMSGCVILFALL 209
Db 250 KNRRIKIADFGMAALEPNKLLKTS CGSPHVASPEIVMGRPVHGGPSDVMSCGIVLFALL 309
QY 210 VCALEPDDNLEFOLLEKVKRGVFMHPHTPPDCQLLRGMIEVREKELSLQIOKHPW- 268
Db 310 TGHLPFDDNDNIKKLLLLKQSGKIQMPNSLSEAROLISKILVIDPEKRITTEILKHPLI 369
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QY 269 -----YLGKHEPPCPEAPGRRVAMKSLPSNGELDDPDVLESMA 309
Db 370 KKYDDL PVNKVLKMKRKONMARGKNSD--LHLLNNVSPSIVTLHSGKEIDSEILRSQI 427
QY 310 LCFDRDRRLHRELSEENQEKMIYYILLDKERY-----PSCEDQDLPPNDVDPKPK 364
Db 428 LHWGVSRELIITAKLQKPMSEBKJFYLLQYKQHSISLSSSSSENKKSATSESSVNEPRI 487
QY 365 RYDSPMLSRHGKRRPERKSMELVSLITDAGGGSPVPTRRALMAHQSHQ-----RSRSVS 418
Db 488 EVASKTANNYGLR-----SENNDVKTLHSLLEI--HSEDTSTVNQNNAIT 529
QY 419 GASTGL-----SSSPLSSPRS-----PVFSPSPGAGDEARGG 453
Db 530 GVNTEINAPVLAQKQSFINTLSQPESDKAEAEAVTLPPAIPFNAS-----SSRIFR 582
QY 454 SPISKQTQTLPSRPGGAGEQPPPSARST-----PLPGGPGSP-----RSGGTP 500
Db 583 NSYTSISRSRSLRLSLNSRLSASSTRETVHDNEMPLPQLPKSPRSYLSERRAIHASP 642
QY 501 ----LHSPHLTPRASPTGTPPTPPSPGGVGGAAMRSRLNSI--RNSFLGSPFRHRRKM 555
Db 643 STKSIHKSLSRKNIAAT-----VAARRTLQNSASKRSLSYLSQISIKRSL 686
QY 556 QV-----PTAEMSSLTPESSPE-----LAKRSWFGNFIS--LDKEEQIF 593
Db 687 NLNDLIVFPDPLPSPKPPASENVKSPHSLSDSDFEILCDQILFGNALDRILEEED-- 744
QY 594 LVLKDK-----PLSSIKADIHAFSLSPSLSHSVLSQTSFRAEYKA 634
Db 745 ---NEKERTQQRQNDTKSSADTFTTIGSVTNKENGEPY-----TKTEKQFNMYSKP 797
QY 635 SGGPS-----VFQKPVRFQVVISSESGPEPRRDGSGGGIYVTFTLISGSPSRFRK 688
Db 798 SENMGLSFPPIFEK-----ENTLSSSYLEEOKPKR-----AALSDITNSFNKMKQEGMR 848
QY 689 VETIQ-AQLLSTHDPOPSVOALADEKNGAQTRPAGAPPSLQ-----PGRDDEL 739
Db 849 IEKKIQREQLQKNDRPS-----PLKPIQHQLRVLNSLPNDQKPSL 890
QY 740 SSSPRR 745
Db 891 SLDPRR 896

RESULT 3
G01025
serine/threonine protein kinase - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004
C;Accession: G01025
R;Navarro, E.
submitted to the EMBL Data Library, April 1996
A;Reference number: H00564
A;Accession: G01025
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-745 <NAV>
A;Cross-references: UNIPROT:Q15524; UNIPROT:Q96HB3; EMBL:X97630; NID:g1310674
C;Superfamily: protein kinase homology
F;18-271/Domain: protein kinase homology <kin>

Query Match 15.7%; Score 637; DB 2; Length 745;
Best Local Similarity 29.4%; Pred. No. 9.3e-16;
Matches 211; Conservative 92; Mismatches 238; Indels 176; Gaps 28;

QY 91 YLVLEHVS GGELFDYLVKKGRLTPKEARKFRQIVSALDFCHSYISICHRLDKPENLLDE 150
Db 93 YLVMEYASGEVFDYLVHAGRMKEKARAKFRQIVSAVQYCHQKFIVRDLKAENLLDA 152
QY 151 KNRIADFGMASIQVDSGLLETSCGSPHVACPEVKEGYDGRADWMSGCVILFALLV 210
```

Db 153 DMNIKIADFGFSNEFTFGNKLDTCGSPPYAAPBEPFGQKKYDGPEDVWISLGVILYTLVS 212
Qy 211 GALTDDNNLQQLLEKVKRGVHHPHFIPPCQSLRGMIEVEPEKRLSLRQIKHPWYL 270
Db 213 GSLPFDGQNLKELRVLGRKYRIPFYFMSTDCENLLKKFLILNPSKRGTLQIKMDRWNN 272
Qy 271 GQKEPD---PCLRPAPGRRVAMRSLPSNGELDDPVLESMAISGCFDRDRRLHRLRSEE 327
Db 273 VG-HEDDELKYPVPLDYK-----DPRTELWMSG--YTREBIQSLVGQR 317
Qy 328 ENQEKMIYLLLDKRYEYSCEDODLPPRNDVD-----DPRTELWMSG--YTREBIQSLVGQR 317
Db 367 ENQEKMIYLLLDKRYEYSCEDODLPPRNDVD-----DPRTELWMSG--YTREBIQSLVGQR 367
Db 318 YN-EWMAFYLLGVKSSSELEGDTITLKPSPADLTNSSAQFPHKQVRSANPKQRRFS 376
Qy 368 S-----PMLSRHGK-----RRPE-----RKS----- 384
Db 377 DQAGPAIPTSNSYSKKTQSNNAENKRPEDRESGRKASSTAKVPASPPLGLERKKTTP 436
Qy 385 ---EVLSTTDAGGSGSPVTPTRALEMA--OHSORSRSVSG--ASTGLSSSLSPSPSPVF 437
Db 437 STNSVLSTSTWRSNPLERASLQASIQNGKDSLTMPGSRASVASAGVSAAR----- 492
Qy 438 SFSPEPGADGARGGSGSTQTLPSRPGRGGAGEQPPPPSARSTPLPGPPGSP----- 493
Db 493 ---PRHQKSMGSHVHPNKASGLP---PTESNC-EVPRESTA---PQVYPVAPSAHN 540
Qy 494 -RSGGGTP-----LHSPHTPR-----ASPTGTPGTTPPPSPGGVGAARSLN 538
Db 541 ISSGGGAPDRFTNPRGVSSRSTFHAGQLQRVDQONLPGYVTPASPSPGHSQGR--RGASG 598
Qy 539 SIRNSFLGPFHRKQVPTABE-MSSLTP-----ESSPELAKRSW-P 580
Db 599 SIFSKP--TSKVFARNLMEPSKORVETLRPHVVGSGNDKEBEFEAKPRSLRFTWSM 656
Qy 581 GNFTSLQKEQIFLVLDKDKPLSSIKADIVHAFSLSPSLSHSVLSQTSFRAEYKASGGSPV 640
Db 657 KTTSSMEPNEMRIKRVLDANSQSELEKHYMLL--CMHTGPGHEF----- 702
Qy 641 FQKPVRFQVDTSSSEGPSPRRDGGGGGYYVTFTLISGPRFRKRVWETIOAQL 697
Db 703 ----VQWEMEVCCK-----LPRLSLNG-----VRFKRISGTSMAFKNIASKIANEL 743

RESULT 4

JC1446
serine/threonine-specific protein kinase (EC 2.7.1.1.) AK21 - Arabidopsis thaliana
N;Alternate names: protein kinase SNF1 homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JCI446; S58266; S66334
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A;Reference number: JC1446; MUID:93013041; PMID:1339373
A;Accession: JC1446
A;Molecule type: DNA
A;Residues: 1-512 <LEG>
A;Cross-references: UNIPROT:Q38997; GB:M93023; NID:g166599; PIDN:AAA32736.1; PID:g166600
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase genes
A;Reference number: S58266
A;Accession: S58266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 144-198 <THU>
A;Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes
A;Reference number: S66334; MUID:96123233; PMID:8534852
A;Accession: S66334
A;Molecule type: DNA

A;Residues: 144-198 <TH2>
A;Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
C;Comment: This enzyme plays an important role in a signal transduction cascade regulati
C;Genetics:
A;Gene: AK1010; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
Query Match 15.4%; Score 624; DB 1; Length 512;
Best Local Similarity 42.5%; Pred. No. 1.9e-15;
Matches 122; Conservative 59; Mismatches 92; Indels 14; Gaps 4;
Qy 91 YLVLEHVSGLPEFDYLVKGRITPKEARKFPRQIVSALDFCHSYSIHRDLKPNLLIDE 150
Db 93 YLVMEYVNSGELFDYIVKGRITPKEARKFPRQIVSALDFCHSYSIHRDLKPNLLIDE 152
Qy 151 KNNIRIADFGWASLQVGSLSLETSCSPHYACPEVIGKEKYDGRADWMSGCVILFALLV 210
Db 153 KNNIRIADFGWASLQVGSLSLETSCSPHYACPEVIGKEKYDGRADWMSGCVILFALLV 212
Qy 211 GALTDDNNLQQLLEKVKRGVHHPHFIPPCQSLRGMIEVEPEKRLSLRQIKHPWYL 270
Db 213 GALTDDNNLQQLLEKVKRGVHHPHFIPPCQSLRGMIEVEPEKRLSLRQIKHPWYL 272
Qy 271 GQKEPD---PCLRPAPGRRVAMRSLPSNGELDDPVLESMAISGCFDRDRRLHRLRSEE 327
Db 273 A--HLPRYLAVPPPD-----TVQAKKIDEEILQEVINMGF--DRNHILIESLRNRTQND 322
Qy 331 EKMIYLLLDKRYEYSCEDODLPPRNDVDPPKRVDSPLMSR 373
Db 333 EKMIYLLLDKRYEYSCEDODLPPRNDVDPPKRVDSPLMSR 369
RESULT 5
T38929
changed division response protein [validated] - fission yeast (Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38929; T50476
R;Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1997
A;Reference number: 221818
A;Accession: T38929
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-775 <BAD>
A;Cross-references: UNIPROT:P87050; EMBL:Z94864; PIDN:CAB08165.1; GSPDB:GN000066; SPDB:SP
R;Breeding, C.S.; Hudson, J.; Balasubramanian, M.K.; Hemmingsen, S.M.; Young, P.G.; Goul.
Mol. Biol. Cell 9, 3399-3415, 1998
A;Title: The cdr2(+) gene encodes a regulator of G2/M progression and cytokinesis in Sch
A;Reference number: 225082; MUID:99060136; PMID:9843577
A;Accession: T50476
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-775 <BRE>
A;Cross-references: EMBL:AF092508; NID:g3859527; PIDN:AAC72832.1; PID:g3859528
C;Genetics:
A;Gene: SPDB:SPAC57A10.02; cdr2+
A;Map position: 1
C;Function:
A;Description: acts as a mitotic inducer; important for the completion of cytokinesis at
Query Match 15.4%; Score 623.5; DB 2; Length 775;
Best Local Similarity 27.8%; Pred. No. 2.8e-15;

Matches 220; Conservative 109; Mismatches 263; Indels 199; Gaps 30;
QY 34 GNWSFLP-ETHGWSLFLPRINGIVLCHQBPVEVGDALWSSTCFQPSA----- 84
Db 8 GPWELGLSLGSGPNSRLAKHRETQGLAVVKPI-VG-----WSELTSSQQAIEGELVLL 62
QY 85 -----PSI-----SPRVLVLEHVSQGEFLDYLVKKGRLLTPKEAKRFRQIVSALD 129
Db 63 RLLEHNVLIQDIVISAQEQLFVVVEYMPGGEFLFDCMLKRGSTEQDTAKFLWQLCGLE 122
QY 130 FCHSYSTICHRDLKPNLLDEKKNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIKGE 189
Db 123 YCHKLHCHDLKPNLLDAHSGIKIGBFGMASIQPGKLLQTSQSGSPHYASPEIIMGR 182
QY 190 KYGRRADWMSQGVLPALLVGAALPDDDNRLQLEKVKRGVFMHPHFPDQCOSLLRGM 249
Db 183 SYDGCASDIWSCGIIFFALLTGKLPFDDNIRSLLLKVCQGPENSPISPOQHLLYRM 242
QY 250 IEVEPEKRLSLEIQKHPPWYLGKGHPDPCLEPAGRRVAMRSLPNSGELDDPDVLESMA 309
Db 243 LDVDSSTRITWEQIREHFFLSCFVH-----PNISFIILAPIQ-PIDPLIVQHLSL 292
QY 310 L-GCFRDRERLHRELSEENQERMIYLLLDKRYPSCEDQDLPPRNDVDPKRKRVDS 368
Db 293 VFRCSDDPMPLIYELKASQSLVEXTLYTL--SRHLHP-----PSSAAVDRNRAVDD 343
QY 369 PM--LSRHGKRPRPKRMEVLISI-----TDAGGSGSPVETRALEM 407
Db 344 LLGTAASNGQOMDEEREIOAINIPTLAPYPISYAAESVPRPATSAFPLTPVTITSGTFNY 403
QY 408 AQHS-----QRSKSVSGA-----STGLS-----SSPLSSPRSPVFSFSP----- 441
Db 404 SFNAINPOSILQRPATTSVAVPOLPKSVTPCLAYPHDSSMLSNYRPPSALSPPNFNVSI 463
QY 442 -EPG-----AGDEARGGSPKSTQTLPSRPGRGGAGEQPPPPPSARSTPLPG 488
Db 464 NDPEVQLSRRATSLDMSNDFRMNENDPSIVGNLAASNFTTGMG-----PPRKRVTSRME 518
QY 489 PPGS-----PRSSGGTLP-----HSPLHTPRASPT-----GTPCTTP 520
Db 519 HTGNRWVSFPRGSAFNPRTVFNVGNQFNSNINNNYNNQYATWNSRRLTPTS--- 575
QY 521 PPSPGGVGGAARSLRSLIRNSF--LGSPRFRHRKQVPTAEEMSSLTPESSPELAKRS 578
Db 576 -----GERSRADLSQSPASVDSLVNPKHRRRQSLFSPSTKXKLS--GSPFPKRS 625
QY 579 W-----FGNFISLDKEEQIFLVLDKPKLSSIK-ADIVHAFSLIPSLSHVL 623
Db 626 FLRLFSSEPSCKCVYASLVASELEHEILEVLRWQLLGIGIADIYDSVS-ASISARIK 684
QY 624 SQTSPRAEYKASGSPVFKPVRFOVDISSEGEPEPPRRDGGGGGIYSVTFTLISGPS 683
Db 685 QNSLNL-----KPVRFKRSIVIA-----EPPGS-----QAVFVLESQSS 718
QY 684 RRFKRWETIQ 694
Db 719 TTFDLATEFQ 729

RESULT 6

T10449

probable serine/threonine-specific protein kinase (EC 2.7.1.1) - cucumber

N/Alternate names: SNF1-related protein kinase

C/Species: Cucumis sativus (cucumber)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C/Accession: T10449

R/Gumpel, N.J.

submitted to the EMBL Data Library, December 1996

A/Reference number: Z17020

A/Accession: T10449

A/Status: preliminary; translated from GB/EMBL/DBDJ

A/Molecule type: mRNA

A/Residues: 1-504 <GUM>

A/Cross-references: UNIPROT:P93113; EMBL:Y10036
A/Experimental source: cv. Masterpiece; cotyledon

C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine

C/Superfamily: AMP-activated protein kinase; protein kinase homology

C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:6-260/Domain: protein kinase homology <KIN>

Query Match 15.2%; Score 618; DB 2; Length 504;

Best Local Similarity 44.7%; Pred. No. 3e-15; Indels 10; Gaps 3;

Matches 115; Conservative 55; Mismatches 77; Indels 10; Gaps 3;

QY 91 YLVLEHVSQGEFLDYLVKKGRLLTPKEAKRFRQIVSALDFCHSYSTICHRDLKPNLLDDE 150

Db 82 YVMEYKSGELFIVVEKGRLEDEARNFFQIIISGVYCHRNMMVVRDLKPNLLDLS 141

QY 151 KNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIKGEYKGRVDRADWMSQGVLPALLV 210

Db 142 KCVKIADFGLSNIRWDGHLTKTSCGSPNYAAPEVISGLYAGPEVDVWSCGVILYALLC 201

QY 211 GALPPDDNRLQLEKVKRGVFMHPHFPDQCOSLLRGMIEVEPEKRLSLEIQKHPPWYL 270

Db 202 GTLPFDDEINPILFKKIGIYTLPSHSSGARELIPSLMVVDPMKRITIPETIRQHPWFQ 261

QY 271 GKGHPDPCLEPAGRRVAMRSLPNSGELDDPDVLESMAISLGCFRDRERLHRELSEENQ 330

Db 262 A--HLPRYLAVPPP-----TMOQAKKIDEDILQFVVMKGF--DRNQLVESLRNRIQNE 311

QY 331 EKMIYVLLADRKERYPS 347

Db 312 ATVAYVLLDNRFRVSS 328

RESULT 7

T18611

probable serine/threonine-specific protein kinase (EC 2.7.1.1), long splice form - Caenor

N/Contains: probable serine/threonine kinase, short splice form

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T18611; T23144; T23143

R/McMurray, A.

submitted to the EMBL Data Library, October 1996

A/Reference number: Z18997

A/Accession: T18611

A/Status: translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-1192 <WIL1>

A/Cross-references: UNIPROT:Q9TW45; EMBL:Z81027; PIDN:CAB54179.1; GSPDB:GN00023; CESP:H3;

A/Experimental source: clone AH10

A/Accession: T18610

A/Status: translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-487,536-1192 <WIL2>

A/Cross-references: EMBL:Z81027; PIDN:CAB54178.1; GSPDB:GN00023; CESP:H39E23.1b

A/Experimental source: clone AH10

R/McMurray, A.

submitted to the EMBL Data Library, June 1997

A/Reference number: Z19696

A/Accession: T23144

A/Status: translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-1192 <WIL3>

A/Cross-references: EMBL:Z96102; PIDN:CAB54263.1; GSPDB:GN00023; CESP:H39E23.1a

A/Experimental source: clone H39E23

A/Accession: T23143

A/Status: translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-487,536-1192 <WIL4>

A/Cross-references: EMBL:Z96102; PIDN:CAB54262.1; GSPDB:GN00023; CESP:H39E23.1b

A/Experimental source: clone H39E23

C/Genetics:

A/Gene: CESP:H39E23.1a; CESP:H39E23.1b

A/Map position: 5

A; Introns: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 487/3; 535/3; 631/1; 825/2; 914/3; 992/2
C; Keywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific protein kinase, long splice form #8
F; 1-1192/Product: probable serine/threonine-specific protein kinase, long splice form #8
F; 1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short splice form #8

Query Match 15.2%; Score 616; DB 2; Length 1192;
Best Local Similarity 27.3%; Pred. No. 7.5e-15;
Matches 208; Conservative 106; Mismatches 281; Indels 168; Gaps 23;

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Qy 91 YLVLEHVSGGELFDYLVKKGLRTPKEARKFQRIQVSAIDFCHSVSYICHRLDKPENLLDDE 150
Db 243 YLVLEVASGGVFDYLVAGHGRMEKEARKFQRIQVSAVQLSHKNIITHRLDKAENLLDQ 302
Qy 151 KNNIRIADFGWASLQVGDLSLETSCGSPHYACPEVIKGEKVDGRRADWMSGCVILFALLV 210
Db 303 DMNIIKADFGSFTSGNKLDTFCGSPPYAAPLFPQKKYDGPVDVWSLGVILYTLVS 362
Qy 211 GALPFDNDNRQLLEKVRGVFHMHPHIPPDCQSLLRGMIEVEPEKRLSLAQIKHPWYL 270
Db 363 GSLPFDQNLKELRERVLRGKYRIPFYMSTDCENLLKFLVINPQRSSLDNIMKORWMN 422
Qy 271 GKGHEPD--PCLEPAPGRVAMRSLPSNGELDPDVLESMAISLGCFR--DRERLHRELRS 325
Db 423 VGYEDDELKPRIE-----PPKQDIDEQRIEKLQI--FOLGFNKAALLESVEK 468
Qy 326 EENQERKMIYVLLDRKERVPSCE---DQDLPFRNDVDPKRVDSPLMRSHGKRPERK 382
Db 469 EKFDIHATVLLGLERKSDMDASEITMAQSLSHSSINV-----SSSLGQHPAGVITRE 522
Qy 383 SMEVLSITDAGGGSPVPTRRALMAHQSRKSRVSGASTGLSS--SPLSSPSRVPFSF 439
Db 523 --HVTSSAGSSASP-----SRYRSSATATGASTAGSALASANAQHQSSA 571
Qy 440 SPEPGAGDEARGGSPSTKQ---TLPSRGRGGGAGGPPPPSARST-PLPGPPGSPRS 495
Db 572 APSSGSSSRSSQNDAAATAAGGTVMVMSGTRHGQVQMQRAQPTSRQATISLQPPSYKPS 631
Qy 496 SGGT-----PLHSPLHTPRAS---PTGPTGTPPPSPGG-----GVGGAARSLN 538
Db 632 SNTTQIAQIPLFRNRSTSSAAQSPSTGITGTGTRKIDPKGRIPLNSTAVQGHRTGAV 691
Qy 539 SIRNSFLGSPFRHRRKM---QVPTAEEMSSL---TP-----TP-----568
Db 692 AANNGGIPSHRDHAQQOQYQNMQLTSTSTWMSKLNKTPAAGTAATSSSSSSSSATSLAQ 751
Qy 569 -----ESSPELAKRSWFGNF-----TP-----TP-----ISLKEE 590
Db 752 KSGSQISHAPTEPVIREDDDDNNSENQNVPLIGGVGQPTSPAVQVPTEDATSSSDKEQ 811
Qy 591 QIFVLVKDPLSSIKADIVHAFILPSLSHVSLSQTSFRARYKASGGPSVFPQVRVQVD 650
Db 812 QQKASSETPKES-KPSMIHQSPSPMPQMMTAMESLKLSESGQTGGPTV-----860
Qy 651 ISSSEGPEPSRRDGGSGGGIYVTFLLISGSPRRKRVVETIAQALLSHDQPSVALA 710
Db 861 --ATGCP--PQR-----ATSQMGRSATTNANMGSSGGGAAAAASA 898
Qy 711 DEKNGAQTREPAGAPRSLQPPGPRDPSELSSRRGPPPKKL 753
Db 899 TNQLSGAPSTGASSQQYHPKA-----PSSSSSSSTNPPHQHL 937
```

RESULT 8
S27966
N; Alternate names: protein p78
C; Species: Homo sapiens (man)
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C; Accession: S27966
R; Maheshwari, K.K.; Som, S.; Parsa, I.
submitted to the EMBL Data Library, January 1992
A; Description: Sequence of a cDNA encoding 78kD marker protein lost in chemically induced
A; Reference number: S27966

A; Accession: S27966
A; Molecule type: mRNA
A; Residues: 1-713 <W>H>
A; Cross-references: UNIPROT:P27448; EMBL:M80359; NID:g189511; PID:AAAS9991.1; PID:g18951
C; Superfamily: protein kinase homology
C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F; 54-307/Domain: protein kinase homology <KIN>
F; 62-70/Region: protein kinase ATP-binding motif

Query Match 15.0%; Score 608; DB 2; Length 713;
Best Local Similarity 30.4%; Pred. No. 9.1e-15;
Matches 202; Conservative 90; Mismatches 234; Indels 138; Gaps 28;

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Qy 91 YLVLEHVSGGELFDYLVKKGLRTPKEARKFQRIQVSAIDFCHSVSYICHRLDKPENLLDDE 150
Db 129 YLIMEVASGGKVDYLVAGHGRMEKEARKFQRIQVSAVQYCHQKRIVHRLDKAENLLD 188
Qy 151 KNNIRIADFGWASLQVGDLSLETSCGSPHYACPEVIKGEKVDGRRADWMSGCVILFALLV 210
Db 189 DMNIIKADFGSFTSGNKLDTFCGSPPYAAPLFPQKKYDGPVDVWSLGVILYTLVS 248
Qy 211 GALPFDNDNRQLLEKVRGVFHMHPHIPPDCQSLLRGMIEVEPEKRLSLAQIKHPWYL 270
Db 249 GSLPFDQNLKELRERVLRGKYRIPFYMSTDCENLLKFLVINPQRSSLDNIMKORWMN 308
Qy 271 GKGHEPD--PCLEPAPGRVAMRSLPSNGEL---DPDVLESMAISLGCFRDRERLHREL 324
Db 309 AG-HEEDELKPFVEP-----ELDISDQKIDIMVGMG-----Y 340
Qy 325 SEENQERKMIYVLLDRKERVPSCE---DQDLPFRNDVDPKRVDSPLMRSHGKRPERK 370
Db 341 SQSEIQESLSKMKYDEITATYLLGRK-----SSEVRPSSDLNNTGSPPHHKVQSV 393
Qy 371 LSRHGKRPRPKSMVLSITDAGGGSP---VPTRRALMAHQSRQ---SRSVSGAS 421
Db 394 SSSQKQRR-----YSDHAGPGIPSVVAYPKRSQTSADSLKEDGISSRKSTGSA 443
Qy 422 TGLSSPSLSPRSPVPSFSPGAGDEARGGSPSTKQTLPSRGRGGGAGGPPPPSA 481
Db 444 VGGKG---TAPASPMILGNASNPNKADIPE-----RKKSSTVPSSNTASGGM-----TR 488
Qy 482 RSTPLPCPPGSPSSSGTGLHSPHTPRASPTGCTTPPTPPSPCGGVGGGAARSL-----537
Db 489 RNTYV---CSERTTDDR--HSVIQNGKENST-IPQORTPVASTHSSAATPDRIAPPR 541
Qy 538 -NIRNSFLGSPFRHRRKMVPTAEEMSSLTPSSPELAKRS-----WFGNFIIS-LDKEE 590
Db 542 GTASRSTFHQQR-ERRATYNGPPASPSLSHVSLSQTSFRSGSTTLFSLKLSKLTSTR 600
Qy 591 QIFVLVKD-----KPLS-----SIK-----ADIVHAFILPSLSHVSLSQTSFRARYK 633
Db 601 NVSAKQKDEKNEKAPKSLRFTWMSKNTTSSMDPGDMMREIRKVLDDANNCDYEQRE-RFLLF 659
Qy 634 ASGGPSVFPQVRVQVDISSESEGPSPRDRDGGGGIYVTFLLISGSPRRKRVVETI 693
Db 660 CVHGDGHAENLVQWMEVCK-----LPLRLSLNG-----VRPKRISGTSIAFKNIASKI 707
Qy 694 QAQL 697
Db 708 ANEL 711
```

RESULT 9
S59359
N; Alternate names: protein YDR507c
C; Species: Saccharomyces cerevisiae
C; Date: 30-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004
C; Accession: S59359; S69565
R; Longtine, M.S.; Pringle, J.R.
submitted to the EMBL Data Library, August 1995
A; Reference number: S59359
A; Accession: S59359

A;Molecule type: DNA
A;Residues: 1-1142 <LON>
A;Cross-references: UNIPROT:Q12263; EMBL:U331140; NID:g992650; PIDN:AAA75513.1; PID:g992650
R;Dietrich, F.S.
Submitted to the EMBL Data Library, August 1995
A;Description: The sequence of S. cerevisiae cosmids 8166, 9787, 9717, and lambda 3073.
A;Reference number: S69553
A;Accession: S69565
A;Molecule type: DNA
A;Residues: 1-1142 <DIE>
A;Cross-references: EMBL:U33057; NID:g927764; PIDN:AAB64949.1; PID:g927777; MIPS:YDR5070
C;Genetics:
A;Gene: SGD:GIN4
A;Cross-references: SGD:S0002915; MIPS:YDR507c
A;Map position: 4R
C;Superfamily: protein kinase homology
C;Keywords: ATP
F;17-289/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif

Query Match 14.9%; Score 604; DB 2; Length 1142;
Best Local Similarity 39.0%; Pred. No. 1.9e-14;
Matches 152; Conservative 54; Mismatches 118; Indels 66; Gaps 12;

QY 91 YLVLEHVSQGELEFDYLVKKGRLTPKEARKPFQIVSALDFCHSYISCHRDLPENLLDDE 150
DB 107 YLVLEYAEKGELEFDYLVKKGRLTPKEAIRPFQIIIGVSYCHALGIVHRDLKPENLLD 166

QY 151 KNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIGKEKYGRRADWMSGCVILFALLV 210
DB 167 KYNKIADFGMALETGKLETSKSGSPHYAAPVIGPIYQGFASDVMSGCVILFALLT 226

QY 211 GALPPD--DDNLRQLLEKVGKGFHMP--HFIPDCCQLLRGMIEVEPEKRLSLEQIQKH 266
DB 227 GRLPDEEDGNIRTLKLVKQGEFMSDDISREAOQLKILTVDPERRIKTRDILKH 286

QY 267 PWYLGKHEPDPCLPAPGRR--VAMRSLP-----SNGELPDVLESMAISGCF 313
DB 287 -----PQQKYSIRDSKIRGLPREDIYVLTPLSESSSIDATILQNLVILMHG 335

QY 314 RDRERLHRELSEENQEMKIYLLDRKERYPCSE-----DQDLPFRNDVD---PP 362
DB 336 RDEGIGKEKLEPGANAETLYALYRFK-----CDTQKELIKQQQVKKQSSVSVSP 390

QY 363 RKRVDSPMLSRHGKRPKRKMEVLSITDAGGGSPVPTRALEMAQHSQRSVSGAST 422
DB 391 SKKV-----STPQRRNRRESU--ISVTSS-----RKPIFNKFTASSSSNLT 435

QY 423 GLSSSPLSGSPRSP-----VFSFSPPECA 445
DB 436 PGSSKRLSKNFSSKKLSTIVNQSSPTPAS 465

RESULT 10
T07788
probable serine/threonine-specific protein kinase (EC 2.7.1.1-) SNF1 - potato
N;Alternate names: StubSNF1 protein
C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07788
R;Lakatos, L.; Banfalvi, Z.
submitted to the EMBL Data Library, January 1997
A;Reference number: Z16133
A;Accession: T07788
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-512 <LAK>
A;Cross-references: UNIPROT:O04122; EMBL:U83797; NID:g1935915; PIDN:AAB52224.1; PID:g1935915
C;Genetics:
A;Gene: SNF1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: AMP-activated protein kinase; protein kinase homology

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>

Query Match 14.8%; Score 599; DB 2; Length 512;
Best Local Similarity 43.6%; Pred. No. 1.4e-14;
Matches 116; Conservative 53; Mismatches 83; Indels 14; Gaps 4;

QY 91 YLVLEHVSQGELEFDYLVKKGRLTPKEARKPFQIVSALDFCHSYISCHRDLPENLLDDE 150
DB 93 YVMEYVKSGELEFDYIVEKGRLEQDEARNFFQIIISGVYCHINMVVHRDLKPENLLD 152

QY 151 KNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIGKEKYGRRADWMSGCVILFALLV 210
DB 153 KNNVKIADFGLSNIMRDGHFLKTCGSPNYAAPVIGKLYAGVEVDVMSGCVILYALLC 212

QY 211 GALPPDDNLRQLLEKVGKGFHMPHPTPPDCCQLLRGMIEVEPEKRLSLEQIQKHFWYL 270
DB 213 GTLPDDDENIPNLFKIKGGYITLPSHLSAGARDLIPRMLIVDPKMTIPEIRLHFWFQ 272

QY 271 GQKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISGCFRDRERLHRELSEENQ 330
DB 273 A--HLPRYLAVPPD-----TMOQAKKIDBEILQEVVKGMF--DRNNLTESLRNVQNE 322

QY 331 EKMYYILLDRKER-----YPSCEDQD 352
DB 323 GTVPYYLLDNRHVRVSTGYLGAEPQE 348

RESULT 11
G89287
protein H39E23.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: G89287
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology,
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G89287
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1246 <STO>
A;Cross-references: GB:chr_V; PIDN:CAB09532.1; PID:g3878100; GSPDB:GN00023; CESP:H39E23.1
C;Genetics:
A;Gene: H39E23.1
A;Map position: 5

Query Match 14.7%; Score 598; DB 2; Length 1246;
Best Local Similarity 28.2%; Pred. No. 3.3e-14;
Matches 204; Conservative 103; Mismatches 268; Indels 148; Gaps 24;

QY 91 YLVLEHVSQGELEFDYLVKKGRLTPKEARKPFQIVSALDFCHSYISCHRDLPENLLDDE 150
DB 133 YLVLEVASGGEVDYLVHGRMKEKARAKFRQIVSAVQYLSKNTIHRDLKAENLLDQ 192

QY 151 KNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIGKEKYGRRADWMSGCVILFALLV 210
DB 193 DMNIKIADFGSFTNSIGNKLDTPCGSPYAAPVIGKLYAGVEVDVMSGLVILYTLVS 252

QY 211 GALPPDDNLRQLLEKVGKGFHMPHPTPPDCCQLLRGMIEVEPEKRLSLEQIQKHFWYL 270
DB 253 GSLLPFDQNLKELRERVLKRYRPFVMTSDCNLLKFLVINVPPQRSSLDNIMDRWMN 312

QY 271 GQKHEPD--PCLEPAPGRRVAMRSLPSNGELDPDVLESMAISGCFR--DRELRHRELRS 325
DB 313 VGYEDDELKPFIE-----PPDQIQIDEQRIEKLQI--FQGFNKAAILSEVEX 358

QY 326 EENQERKMYYLLDRKERYPCSE-----DQDLPFRNDVDPPKRVDSPLSRHGKRPKR 382
DB 359 EKFDIATYLLIGERKSDMDASEITWAQSLSHSSINV-----SSSLQHPAGVITRE 412

Db 91 YVWMEYKSGELFDYIVKGRLOEDBARKI FQOI IAGVYCHKNMVVHRDLKPENLLIDA 150
Qy 151 KNNIRIADFGMASLQVDSLETSCGSPHYACPEVKGKYGDRRADMSWCGVILFALLV 210
Db 151 RNNVKIADFGNIMRDGHFLKTS CGSPNVAAPVGVSGKLYAGPEVDVWSCGVILYALLC 210
Qy 211 GALPFDNDNLRLLEKVKRGVFMHPIPPDCQSLRGMIEVEPEKRLSLEQIQKHPWYL 270
Db 211 GTLPFDNDENIPNFKIKSGVYTLPSHLSPALDLPRLMLVDPMKRIISVPDIRQWTF- 269
Qy 271 GKGHEPDCLEPAPGRVAMRSLPSNGELDPDVLESMAISLGCFFRDRERLHRLRSEENQ 330
Db 270 -KIHLPYLA VPPDARQHLK-----KLDDEILQVSRMGL--DRDQLDLSLQKXIQDD 320
Qy 331 EKMIYLLDRKERYPS-----CEDODLPFRNDVDPKRVDPSPMLSRHGKR 378
Db 321 ATWAYILLYDNRSMASSGVLGAERFQESVDCVSPGLFPNLDL---QLSTGNGVSESSLR 376
Qy 379 PERK 382
Db 377 PERK 380
RESULT 14
T29858
hypothetical protein T01C8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29858
R:Wohldmann, P.; Hawkins, J.
A:Submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid T01C8.
A:Reference number: 220699
A:Accession: T29858
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-562 <WOH>
A:Cross-references: UNIPROT:Q22068; EMBL:U58726; PIDN:AAB00579.1; GSPDB:GN00028; CESP:TQ
A:Experimental source: strain Bristol N2; clone T01C8
C:Genetics:
A:Gene: CESP:T01C8.1
A:Map position: X
A:Introns: 41/1; 197/2; 237/1; 272/2; 307/3; 375/1; 479/1; 529/3
C:Superfamily: AMP-activated protein kinase; protein kinase homology
Query Match 14.7%; Score 595; DB 2; Length 562;
Best Local Similarity 31.0%; Pred. No. 2.1e-14;
Matches 161; Conservative 65; Mismatches 146; Indels 148; Gaps 15;
Qy 83 SAPSISFRYLVLHVSGGELFDYLVKKGRLTPKEARKFQIIVSALDFCHSYISICHRLDLK 142
Db 93 STPSDIF--WMEHVSGGELFDYIVKGRKLTAEARRFQOIISGVYCHRMVVRDLK 150
Qy 143 PENLLDEKNNIRIADFGMASLQVDSLETSCGSPHYACPEVKGKYGDRRADMSWCG 202
Db 151 PENLLDEKNNIADFGLSNIMTDCGLRFTSCGSPNVAAPVSGKLYAGPEVDVWSCG 210
Qy 203 VILFALLVGNALPDDNDNLRLLEKVKRGVFMHPIPPDCQSLRGMIEVEPEKRLSLEQ 262
Db 211 VILYALLCGTLPPDDSHVPSLFRKISGVFPPTDFLERIVNLLHMLCVDPMKATIKD 270
Qy 263 IQKHPWYLGKGHEPDCLEPAPGRVAMRSLPSNGELDPDVLESMAISLGCFFRDRERLH 321
Db 271 VIAHEWF-----QKDLFN--YLFPPISEASIVDIEAVREVT 308
Qy 322 ELRSEENQEKMI-----YVILLDRKERYSCEDQDLPPRNDVDPKRVDPSPMLSRHGKR 370
Db 309 YHVAEEVTSALLGDDPHHLSLAYNLIVDNKRIADETAKLSIEEFYVTP--NKGPGV 366
Qy 371 LSRHGKRPER-----KSMVLSITDAGGG----- 396
Db 367 -----HRHPRIASVSSKITPTILDNTEASGANENKRAKWHLGIRSQSRPEDIMPEVFRA 421

Qy 397 -----SPV--PTRRALEMAQHSQRS-----RVSGASTGLSS 426
Db 422 MKQLDMKWKVLPVHVIVRRKPDAPADPPKMSLQLYQVDRSYLLDFKSLADEESGAS 481
Qy 427 SPLSSPSPVSPFSPGAGDEARGGSPSTKVTQLPSRGRGGGAGEQPPPSARSTPL 486
Db 482 A--SSSRHASMPQKPA-----GIRG-----TRTSSM 507
Qy 487 PGPGSPRSGGTPLHSPHLPTRASPTGTGTTPPPSPGG 526
Db 508 POAMSMEASIEKMEVHD-----FSDMSCDVTPPPSPGG 540
RESULT 15
S59941
serine/threonine-specific protein kinase (EC 2.7.1.-) BKIN2 - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: S59941
R:Hannappel, U.; Vicente-Carabajosa, J.; Barker, J.H.A.; Shewry, P.R.; Halford, N.G.
A:Plant Mol. Biol. 27, 1235-1240, 1995
A:Title: Differential expression of two barley SNF1-related protein kinase genes.
A:Reference number: S59941; MUID:95284374; PMID:7766906
A:Accession: S59941
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-473 <HAN>
A:Cross-references: UNIPROT:Q43475; EMBL:X82548
C:Genetics:
A:Gene: BKIN2
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:1-244/Domain; protein kinase homology (fragment) <KIN>
F:21,40,115,117/Active site: Lys, Glu, Asp, Lys #status predicted
F:120,124/Binding site: magnesium (Asn, Asp) #status predicted
Query Match 14.7%; Score 594.5; DB 1; Length 473;
Best Local Similarity 38.6%; Pred. No. 1.9e-14;
Matches 127; Conservative 60; Mismatches 103; Indels 39; Gaps 7;
Qy 91 YLVLEHVSGGELFDYLVKKGRLTPKEARKFQIIVSALDFCHSYISICHRLDLKPENLLDE 150
Db 66 YVWMEYKSGELFDYIVKGRLOEDBARKI FQOI IAGVYCHKNMVVHRDLKPENLLIDS 125
Qy 151 KNNIRIADFGMASLQVDSLETSCGSPHYACPEVKGKYGDRRADMSWCGVILFALLV 210
Db 126 KCVKIADFGLSNIMRDGHFLKTS CGRPNVAAPVSGKLYAGPEVDVWSCGVILYALLC 185
Qy 211 GALPFDNDNLRLLEKVKRGVFMHPIPPDCQSLRGMIEVEPEKRLSLEQIQKHPWYL 270
Db 186 GTLPFDNDENIPNFKIKSGIYTLPSHLSPALDLPRLMLVDPMKRIIRIAREHSWFK 245
Qy 271 GKGHEPDCLEPAPGRVAMRSLPSNGELDPDVLESMAISLGCFFRDRERLHRLRSEENQ 330
Db 246 A--RLPYLA VPPDPTAQVK-----KLDDETLNDVIMKGF--DKNQLTSLQKQLONE 295
Qy 331 EKMIYLLDRKER-----YPSCEDQDLPPRNDVDPKRVDPSPMLSRHGKRPERKSMEV 386
Db 296 ATWAYILLYDNKRLTTSVGLGAEYQ-----SMDSSFSQISPETFS--- 336
Qy 387 LSITDAGGSPVPTRRALEMAQHSQRSR 415
Db 337 -SASEARQYGGP-----GFGLRQHFAAER 359
Search completed: February 17, 2005, 11:03:26
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 10:30:05 ; Search time 179 Seconds
(without alignments)
2179.913 Million cell updates/sec

Title: US-10-803-277-4

Perfect score: 4056

Sequence: 1 MGLEFGLEAGNWSHPLPG.....PRRGPPKDKLLATNGTLP 762

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3545	87.4	794	1 K111_HUMAN	Q8tdc3 homo sapien
2	3518	86.7	776	2 Q699J6	Q699J6 mus musculu
3	2405	59.3	719	2 Q699J3	Q699J3 mus musculu
4	2400	59.2	766	2 Q6ZMQ4	Q6ZMQ4 homo sapien
5	2397	59.1	705	2 Q69298	Q69298 mus musculu
6	2390.5	58.9	675	2 Q699J4	Q699J4 mus musculu
7	2386	58.8	736	1 ST29_HUMAN	Q8iwd3 homo sapien
8	2379.5	58.7	653	2 Q6DMN7	Q6dmn7 mus musculu
9	2188.5	54.0	523	2 Q6PHM0	Q6phm0 mus musculu
10	1588	39.2	861	2 Q9VUV4	Q9vuv4 drosophila
11	1571.5	38.7	696	2 Q7PV95	Q7pv95 anopheles g
12	1438	35.5	698	2 Q61298	Q61298 halocynthia
13	1383	34.1	914	2 Q19469	Q19469 caenorhabdi
14	1228	30.3	701	2 Q95T82	Q95t82 drosophila
15	731	18.0	1058	2 Q6C6T2	Q6c6t2 yarrowia li
16	693	17.1	1425	2 Q75D01	Q75dq1 ashbya goss
17	677	16.7	1518	1 KKK1_YEAST	P34244 saccharomyc
18	658	16.2	833	2 Q76P07	Q76p07 dictyosteli
19	651.5	16.1	1311	2 Q6P486	Q6p486 mus musculu
20	647	16.0	1314	2 Q6B125	Q6bt82 debaryomyce
21	646.5	15.9	1267	2 Q6CK49	Q6ck49 kluyveromyc
22	646.5	15.9	1267	2 Q72865	Q72865 kluyveromyc
23	643.5	15.9	764	2 Q6ZNL8	Q6znl8 homo sapien
24	643.5	15.9	783	2 Q86YJ2	Q86yj2 homo sapien
25	643	15.9	1531	2 Q6B125	Q6bt82 debaryomyce
26	637	15.7	691	2 Q96RG0	Q96rg0 homo sapien
27	636	15.7	745	2 Q15524	Q15524 homo sapien
28	636	15.7	755	2 Q7KZ17	Q7kzi7 homo sapien
29	636	15.7	778	2 Q96HB3	Q96hb3 homo sapien
30	632.5	15.6	1187	2 Q6NSH8	Q6nsh8 brachydanio
31	632	15.6	722	2 Q6PDR4	Q6pdr4 mus musculu

RESULT 1

ID	K111_HUMAN	STANDARD	PRT	794 AA
AC	Q8TDC3; Q8NDD0; Q8NDR4; Q8TDC2; Q96AV4; Q96JL4;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	03-JUL-2004 (Rel. 44, Last annotation update)			
DE	Probable serine/threonine-protein kinase KIAA1811 (EC 2.7.1.37).			
GN	Name=KIAA1811;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Brain;			
RA	She X.Y., Yu L., Guo J.H.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
[2]				
RP	SEQUENCE OF 51-794 FROM N.A.			
RC	TISSUE=Brain;			
RA	Koehler K., Beyer A., Bloeker H., Boecher M., Brandt P., Mewes H.-W.,			
RA	Weil B., Wiemann S.;			
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.			
[3]				
RP	SEQUENCE OF 80-794 FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=212451130; PubMed=11347906;			
RA	Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. XX.			
RT	The complete sequences of 100 new cDNA clones from brain which code			
RL	for large proteins in vitro.";			
RL	DNA Res. 8:85-95(2001).			
[4]				
RP	SEQUENCE OF 303-794 FROM N.A.			
RC	TISSUE=Lymph;			
RX	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.H.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J.J., Hulton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			

ALIGNMENTS

32	632	15.6	752	1 MKK4_HUMAN	Q96L34 homo sapien
33	632	15.6	752	2 Q8NG37	Q8ng37 homo sapien
34	631.5	15.6	1189	2 Q6PHV1	Q6phv1 brachydanio
35	631	15.6	722	2 Q08679	Q08679 rattus norv
36	630.5	15.5	888	2 Q8BR95	Q8br95 mus musculu
37	629.5	15.5	1489	2 Q6PMF3	Q6fmf3 candida gla
38	629	15.5	1371	2 Q9Y2K2	Q9y2k2 homo sapien
39	628	15.5	786	1 SN1L_HUMAN	P57059 homo sapien
40	626.5	15.4	719	2 Q68A18	Q68a18 homo sapien
41	624	15.4	535	1 K1L0_ARATH	P87050 arabidopsis
42	623.5	15.4	775	1 CDR2_SCHPO	P87050 echinosacch
43	622	15.3	542	2 Q6V8Y5	Q6v8y5 physcomitre
44	621.5	15.3	785	2 Q8QGV3	Q8qgv3 xenopus lae
45	621	15.3	634	2 Q80T81	Q80t81 mus musculu

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=Q8TRDC3-1; Sequence=Displayed;
Name=2;
IsoId=Q8TRDC3-2; Sequence=VSP_008158;
-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-1- SIMILARITY: Contains 1 UBA domain.
-1- CAUTION: Ref.2 (CAD38950) sequence differs from that shown due to a frameshift in position 781.

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EMBL; AF479826; AAL87697.1; -;
EMBL; AF479827; AAL87698.1; -;
EMBL; AL834275; CAD38950.1; ALT_FRAME.
EMBL; AL831945; CAD38595.1; -;
EMBL; AB058714; BAB47440.1; -;
EMBL; BC016681; AAH16681.1; ALT_INIT.
HSP; Q63450; IAO6.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR000449; UBA.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00030; UBA; 1.
KW Alternative splicing; ATP-binding; Serine/threonine-protein kinase;
Transferase.
FT DOMAIN 50 301 Protein kinase.
FT DOMAIN 330 372 UBA.
FT DOMAIN 508 556 Pro-rich.
FT NP_BIND 56 64 ATP (By similarity).
FT BINDING 79 79 ATP (By similarity).
FT ACT_SITE 172 172 Proton acceptor (By similarity).
FT VARSP_LIC 1 42 MVAGLTGKGPSPDGVSPERKDVAGGGGEAEABERG
R -> MSSGAKSGGGSPAYLHPHPHPQPQ (in isoform 2). 068158.
/FTID=VSP_008158.
FT CONFLICT 778 778 G -> A (in Ref. 4).
FT SEQUENCE 794 AA; 86753 MW; 5DD395B0E61AEF77 CRC64;
Query Match 87.4%; Score 3545; DB 1; Length 794;
Best Local Similarity 99.7%; Pred. No. 5e-130; 1; Indels 0; Gaps 0;
Matches 672; Conservative 1; Mismatches 0;
QY 89 FRYLVLEHVSGGELFDYLVKKGRLTPKEARKFRRQIVSALDFCHSYSI CHRLDKPENLLL 148
DB 121 YLYLVLEHVSGGELFDYLVKKGRLTPKEARKFRRQIVSALDFCHSYSI CHRLDKPENLLL 180
QY 149 DEKNRIADFGMASLVQGSLLTSCGSPHYACPEVIKGEKYDGRADWNSGVILFAL 208
DB 181 DEKNRIADFGMASLVQGSLLTSCGSPHYACPEVIKGEKYDGRADWNSGVILFAL 240
QY 209 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPPDQCSSLRGMI EPEPEKLSLEQIQKHPW 268
DB 241 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPPDQCSSLRGMI EPEPEKLSLEQIQKHPW 300

QY 269 YLGKHEPDCLEPAPGRRVAMESLPSNGELDPDVLESMAISLGCFFDRDRRLHRELSEEE 328
DB 301 YLGKHEPDCLEPAPGRRVAMESLPSNGELDPDVLESMAISLGCFFDRDRRLHRELSEEE 360
QY 329 NQEMIIYLLLDKERYPSCEDQDLPRNDVDPKRKVDSPMLSRHGKRRPERKSEVL 388
DB 361 NQEMIIYLLLDKERYPSCEDQDLPRNDVDPKRKVDSPMLSRHGKRRPERKSEVL 420
QY 389 ITDAGGGSSVPTRRALEMAHQSRVSAGSTGLSSSLSPSPRSPVFSFSPGAGDE 448
DB 421 ITDAGGGSSVPTRRALEMAHQSRVSAGSTGLSSSLSPSPRSPVFSFSPGAGDE 480
QY 449 ARGGSPTSQTQTLPSRPGGGAGGEP PPPSARSTPLPGPGSPRSSGGTPLHSLHTP 508
DB 481 ARGGSPTSQTQTLPSRPGGGAGGEP PPPSARSTPLPGPGSPRSSGGTPLHSLHTP 540
QY 509 RASPTGPTGTPPPSPGGVGGAAWRSLNIRNSFLGSPFRHRRKMQVPTAEEMSLTP 568
DB 541 RASPTGPTGTPPPSPGGVGGAAWRSLNIRNSFLGSPFRHRRKMQVPTAEEMSLTP 600
QY 569 ESSPELAKRSWFGNFISLDKEEQIFVLKDKPLSSIKADIVHAFSLSPSLSHSVLSQTSF 628
DB 601 ESSPELAKRSWFGNFISLDKEEQIFVLKDKPLSSIKADIVHAFSLSPSLSHSVLSQTSF 660
QY 629 RAEYKASGGSPVFKPVRFOVDISSSEGEPEPSPRDGGGGIYSVTFTLISGSPRRFKR 688
DB 661 RAEYKASGGSPVFKPVRFOVDISSSEGEPEPSPRDGGGGIYSVTFTLISGSPRRFKR 720
QY 689 VVETIQALLSHDQPSVQALADENKGAQTRPAGAPPSRLOPPGPRDPPELSSPRGPP 748
DB 721 VVETIQALLSHDQPSVQALADENKGAQTRPAGAPPSRLOPPGPRDPPELSSPRGPP 780
QY 749 KDKKLLATNGTLP 762
DB 781 KDKKLLATNGTLP 794
RESULT 2
Q699J6 PRELIMINARY; PRT; 776 AA.
ID AC Q699J6
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative serine/threonine kinase SADB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kishi M., Sanes J.R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC EMBL; AY533671; AAT08446.1; -;
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00030; UBA; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase;
SQ SEQUENCE 776 AA; 84920 MW; EAC59E8740C159D8 CRC64;

Query Match 86.7%; Score 3518; DB 2; Length 776;
Best Local Similarity 99.0%; Pred. No. 5.5e-129;
Matches 667; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 89 FRYLVLEHVS GGLFDYLVKKGRITPKAEKFRQIVSALDFCHSYISICHRDLKPENLL 148
DB 103 YLYLVLEHVS GGLFDYLVKKGRITPKAEKFRQIVSALDFCHSYISICHRDLKPENLL 162
QY 149 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIGKGYDGRADWMSCGVILFAL 208
DB 163 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIGKGYDGRADWMSCGVILFAL 222
QY 209 LVGALPDDNNLQRLLEKVKRGVFMHPHFTIPPCQSLLRGMIEVEPKRLSLQIQHPW 268
DB 223 LVGALPDDNNLQRLLEKVKRGVFMHPHFTIPPCQSLLRGMIEVEPKRLSLQIQHPW 282
QY 269 YLGGKEHPDCLPAPGRVAMSLPSNGELDDPVLSEMASLGCFRDRRLHRLRSEEE 328
DB 283 YLGGKEHPDCLPAPGRVAMSLPSNGELDDPVLSEMASLGCFRDRRLHRLRSEEE 342
QY 329 NQEKMIYLLLDKRYEYPCEDQDLPPRNDVDPKRVDSFPMLSRHGKRPERKSMVLS 388
DB 343 NQEKMIYLLLDKRYEYPCEDQDLPPRNDVDPKRVDSFPMLSRHGKRPERKSMVLS 402
QY 389 ITDAGGGSPVPTTRALEMAHQSRSSVSGASTGLSSPLSPSPVFSPEPGAGDE 448
DB 403 ITDAGGGSPVPTTRALEMAHQSRSSVSGASTGLSSPLSPSPVFSPEPGAGDE 462
QY 449 ARGGSPTSQTOTLPSRGRGGGAGQPPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 508
DB 463 ARGGSPTSQTOTLPSRGRGGGAGQPPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 522
QY 509 RASPTGTPTTTPPSGGVGGAAWRSLNRSIRNSFLGSPFRHRRKMQVPTAEEMSLTP 568
DB 523 RASPTGTPTTTPPSGGVGGAAWRSLNRSIRNSFLGSPFRHRRKMQVPTAEEMSLTP 582
QY 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFPLSPISLSHVSLSQTSF 628
DB 583 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFPLSPISLSHVSLSQTSF 642
QY 629 RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGGIYVTFTLISGFSRFRKR 688
DB 643 RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGGIYVTFTLISGFSRFRKR 702
QY 689 VVETIOAQLLSTHDQPSVQALADEKNGAQTTPAGAPRSLQPPDPDELSSSPRGPP 748
DB 703 VVETIOAQLLSTHDQPSVQALADEKNGAQTTPAGAPRSLQPPDPDELSSSPRGPP 762
QY 749 KDKKLLATNGTTPLP 762
DB 763 KDKKLLATNGTTPLP 776

RESULT 3

Q699J3 PRELIMINARY; PRT; 719 AA.
ID Q699J3
AC Q699J3
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Putative serine/threonine kinase SADA gamma.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kishi M., Sanes J.R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; AV533674; AAT08449.1; --
DR GO:0005524; F:ATP binding; IEA.
DR GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000719; prot kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR InterPro: IPR008271; Ser_Thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR ProDom: PD000001; Prot kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 719 AA; 79938 MW; 4C2ABA57205974AB CRC64;

Query Match 59.3%; Score 2405; DB 2; Length 719;
Best Local Similarity 69.3%; Pred. No. 6.9e-86;
Matches 481; Conservative 55; Mismatches 64; Indels 94; Gaps 11;

QY 89 FRYLVLEHVS GGLFDYLVKKGRITPKAEKFRQIVSALDFCHSYISICHRDLKPENLL 148
DB 91 YLYLVLEHVS GGLFDYLVKKGRITPKAEKFRQIVSALDFCHSYISICHRDLKPENLL 150
QY 149 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIGKGYDGRADWMSCGVILFAL 208
DB 151 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIGKGYDGRADWMSCGVILFAL 210
QY 209 LVGALPDDNNLQRLLEKVKRGVFMHPHFTIPPCQSLLRGMIEVEPKRLSLQIQHPW 268
DB 211 LVGALPDDNNLQRLLEKVKRGVFMHPHFTIPPCQSLLRGMIEVEPKRLSLQIQHPW 270
QY 269 YLGGKEHPDCLPAPGRVAMSLPSNGELDDPVLSEMASLGCFRDRRLHRLRSEEE 328
DB 271 YLGGKEHPDCLPAPGRVAMSLPSNGELDDPVLSEMASLGCFRDRRLHRLRSEEE 328
QY 329 NQEKMIYLLLDKRYEYPCEDQDLPPRNDVDPKRVDSFPMLSRHGKRPERKSMVLS 388
DB 329 NQEKMIYLLLDKRYEYPCEDQDLPPRNDVDPKRVDSFPMLSRHGKRPERKSMVLS 388
QY 389 ITDAGGGSPVPTTRALEMAHQSRSSVSGASTGLSSPLSPSPVFSPEPGAGDE 448
DB 389 VTD---GGSPVARRAIEAQAHQGRSRSISGASSGLSTSLSPR----- 430
QY 449 ARGGSPTSQTOTLPSRGRGGGAGQPPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 508
DB 431 -----VTTPSPRGSPLTPKG-----TPVHTP 453
QY 509 RASPTGTPTTTPPSGGVGGAAWRSLNRSIRNSFLGSPFRHRRKMQVPTAEEMSLTP 568
DB 454 KESPAQTNPPTPSSP--SVGGVPTRLNLSIKNSFLGSPFRHRRKMQVPTAEEMSLTP 511
QY 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFPLSPISLSHVSLSQTSF 628
DB 512 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFPLSPISLSHVSLSQTSF 571
QY 629 RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGGIYVTFTLISGFSRFRKR 688
DB 572 RAEYKATGGGPAVFOKPVRFQVDITYTEGGAQKE-----NGIYSVTFTLISGFSRFRKR 625
QY 689 VVETIOAQLLSTHDQPSVQALA-----DEKNG---AQTTPAGAPRSLQPP 731
DB 626 VVETIOAQLLSTHDQPSVQALSTTNCMEVMTGLSKCKDEKNGQAQAPSTPAKRSAGP 685
QY 732 PGRPDPELSSSPRRGPPKDK-----KLLATNGTP 760
DB 686 -----LGDAAAAGCGDTEYPMGKMAKMGPP 712

RESULT 4

Q6ZMQ4		PRELIMINARY;	PRT;	766 AA.
ID	Q6ZMQ4			
AC	Q6ZMQ4;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Hypothetical protein FLJ16763.			
OS	Homo sapiens (human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID=9606;				
RN	[1]			
CC	SEQUENCE FROM N.A.			
RC	TISSUE=Amygdales;			
RA	Nanmiya K., Wgatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,			
RA	Furuwa T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,			
RA	Katsuha N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,			
RA	Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,			
RA	Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,			
RA	Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,			
RA	Kanehori K., Takahashi-Fujii A., Oshima H., Sugiyama A., Kawakami B.,			
RA	Suzuki Y., Sugano S., Nagahari K., Masuhio Y., Nagai K., Isogai T.;			
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.			
CC	-I- SMIILARY: Belongs to the Ser/thr protein kinase family.			
DR	EMBL; AK315334; BAD18671.1; -.			
DR	HSP; Q63450; 1A06.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.			
DR	GO; GO:0016740; F:transferase activity; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPRO11009; Kinase like.			
DR	InterPro; IPRO00719; Prot.kinase.			
DR	InterPro; IPRO02290; Ser thr.pkinase.			
DR	InterPro; IPRO08271; Ser thr.pkin AS.			
DR	InterPro; IPRO01245; Tyr.pkinase.			
DR	ProDom; PD000001; Prot.kinase; 1.			
DR	SMART; SM00220; S_TRK; 1.			
DR	SMART; SM00219; TyrKc; 1.			
DR	PROSITE; PS00111; PROTEIN KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN KINASE_ST; 1.			
DW	ATP-binding; Kinase: Serine/threonine-protein kinase; Transferase.			
KW	SEQUENCE 766 AA; 84931 NW; BOE5187AF729E947 CRC64;			
SQ				
	Query Match	59.2%;	Score 2400;	DB 2; Length 766;
	Best Local Similarity	68.5%;	Pred. NO. 1.le-85;	
	Matches 475;	Conservative 59;	Mismatches 65;	Indels 94; Gaps 10;
QY	89 FRYLVEHVSGLFDYLVKKGRLLTPKARKFFRIVSALDFCHSYISICHRDLKPENLLL	148		
Db	: :	195		
QY	136 YLYLVEHVSGLFDYLVKKGRLLTPKARKFFRQIIISALDFCHSHSICHRDLKPENLLL	208		
Db	: :	255		
QY	149 DEKNIRIADFVWSLQVSDLSLETSCGSPHYACPEVTIGBKYGRRADMWSCGVILFAL	328		
Db	: :	388		
QY	209 LVGALPFDDNNLRQLLEKVKRGVFHMHPFIIPDCOSLLRGMTVEPKRLSLQIQKHWP	315		
Db	: :	373		
QY	256 LVGALPFDDNNLRQLLEKVKRGVFHMHPFIIPDCOSLLRGMTVEPKRLSLQIQKHWP	328		
Db	: :	388		
QY	269 YLGKGHEPPCLPEPAPGRVAMRSPLNGELDPDVLNSMAGLCFRDRERLHLREURSEE	448		
Db	: :	475		
QY	316 YTGKNEPFP-EQPIP-RKVQIRSLPSLEDIPDVLDMSHSLGCIFRDNRKLQDLLSEEE	373		
Db	: :	448		
QY	329 NQEKMYIYLLDRKERYPCSEDODLPDRNDVDPRKRVDSFMLSGHKPERPKSMVELS	433		
Db	: :	475		
QY	374 NQEKMYIYLLDRKERYPCSEDODLPDRNDVDPRKRVDSFMLSGHKPERPKSMVELS	433		
Db	: : : : : : : : : : ~~~~~~	475		
QY	389 ITDAGGSVPVPTFRRALEMAQHQRSGSVSGASTGLSSPSLSPSPVFSFPCAGDE	448		
Db	: : : : : : : : : : ~~~~~~	475		
QY	434 VTD---GGSPVPAARRALEMAQHQRSGSVSGASTGLSSPSLSPSPVFSFPCAGDE	448		
Db	: : : : : : : : : : ~~~~~~	475		
QY	449 ARGCGSPTSQTLPGRPGGGAGGQQPPPPSARSTPLCPGPCSPRSSCGTPLHSPLHTP	508		
Db	: : : : : : : : : : ~~~~~~	508		

Db	61	YLVLVLEHVS	GCGELFDYLVKKGRLLTPKEARKFFRQIIISALDFCHSHSICHRLDKPENLLL	120	
Qy	149	DEKNIRIAD	FGMASLQVDSLLTSCSGSPHYACPEVIGKEYDGRADWMSCGVILFAL	208	
Db	121	DERNNIRIAD	FGMASLQVDSLLTSCSGSPHYACPEVIRGEKYDGRADWMSCGVILFAL	180	
Qy	209	LVGALPDD	DNLRQLLEKVKGVFHPHFIPDCQSLLRGMIEVPEKRLSLRQIKHPW	268	
Db	181	LVGALPDD	DNLRQLLEKVKGVFHPHFIPDCQSLLRGMIEVDAARRLTLEHIQKHIW	240	
Qy	269	YLGKHEPDP	CLEPAPGRVAMRSLPSNGELDDPVLBSMASLGCGRDRERLHRLSESE	328	
Db	241	YIGGKNEPEP	-EQPIP-RKVQIRSLPSLEDDPVLDSMHSGLGCFDRDNKLLQDLSSESE	298	
Qy	329	NOEKMIYLL	LDKRYPCSDQDLPDRNDVDPPRKVDSPMLSRHGKRPERKSMEVLS	388	
Db	299	NOEKMIYLL	LDKRYPCSHEDQDLPDRNEIDPPRKVDSPMLNRHGKRPERKSMEVLS	358	
Qy	389	ITDAGGSGSP	VPTRRALEMAQHSQRSVSASGLSSPLSSPRSVPFSPSPGAGDE	448	
Db	359	VTD---	GGSPVPARRALEMAHQQRSISGASGLSTSPSSPR-----	400	
Qy	449	ARGGGSPTS	KTQTLPSRGRGGAGEQPPPSARSTPLPGPGSPRSSGGTPLHLSPLHTP	508	
Db	401	-----	-----VTPHSPRGSFLPTPKG-----TPVHTP	423	
Qy	509	RASFTGT	PTPTPPSPGGVGGAAWRSRLNSIRNSFLGSPRFRHRKMQVPTAEMSLLTP	568	
Db	424	KESPA	GTNPPTPPSSP--SVGGVPWRTRLNSIKNSFLGSPRFRHRKMQVPTPEMSNLTP	481	
Qy	569	ESSPELAK	RSWFGNFI	SLDKKEQIFVLVKDKPLSSIKADIVHAFSLPSLSHSVLSQTSF	628
Db	482	ESSPELAK	RSWFGNFI	INLEKEQIFVVIKDKPLSSIKADIVHAFSLPSLSHSVLSQTSF	541
Qy	629	RAEYKAS	GGPSVFQKPVRFQVDISSSEGPSPRRDGGGGGIYSVFTTILSGPSRRFKR	688	
Db	542	RAEYKATG	GPVAVQKPVRFQVDITYTEGGEAQKE-----NGIYSVFTTILSGPSRRFKR	595	
Qy	689	VVETIOA	QLLSTHDQPSVQAL-----ADEKNG- 715		
Db	596	VVETIOA	QLLSTHDQPSVQALSDTTNCMEVMTGRLSKCGTPLSNFFDVIKQLFSDENNGQ	655	
Qy	716	AQTPAGAP	PRSLQPPGRDPELSSSPRGPCKD-----KLLATNGTP 760		
Db	656	AAQAPST	PAKRSAGHP-----LGDAAAAGPGGDTBYPWKGDAWKGMP 698		
RESULT 6					
Q699J4					
ID	Q699J4	PRELIMINARY;	PRT;	675 AA.	
AC	Q699J4;				
DT	25-OCT-2004	(TrEMBLrel. 28, Created)			
DT	25-OCT-2004	(TrEMBLrel. 28, Last sequence update)			
DT	25-OCT-2004	(TrEMBLrel. 28, Last annotation update)			
DE	Putative serine/threonine kinase SADA beta.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Kishi M., Sanes J.R.;				
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.				
CC	-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.				
DR	EMBL:	AY533673; AAT08448.1; -			
DR	GO:	GO:0005524; F:ATP binding; IEA.			
DR	GO:	GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO:	GO:0004713; F:protein-tyrosine kinase activity; IEA.			
DR	GO:	GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro:	IPR011009; Kinase like.			
DR	InterPro:	IPR000719; Prot_kinase.			
DR	InterPro:	IPR002290; Ser_thr_pkinase.			
DR	InterPro:	IPR008271; Ser_thr_pkin_AS.			

DR	InterPro:	IPR001245; Tyr_pkinase.			
DR	ProDom:	PD000001; Prot_kinase; 1.			
DR	SMART:	SM00220; S_TK; 1.			
DR	SMART:	SM00219; TyRK; 1.			
DR	PROSITE:	PS00107; PROTEIN KINASE ATP; UNKNOWN_1.			
DR	PROSITE:	PS00111; PROTEIN KINASE_DOM; 1.			
DR	PROSITE:	PS00108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.				
SQ	SEQUENCE 675 AA; 75361 MW; B01D8D8F9C24C71F CRC64;				
Query Match 58.9%; Score 2390.5; DB 2; Length 675;					
Best Local Similarity 71.9%; Pred. No. 2.4e-85;					
Matches 469; Conservative 54; Mismatches 44; Indels 85; Gaps 9;					
QY	89	FRYLVLVHVS	GGLFDYLVKKGRLTPKEARKFFRQIIISALDFCHSHSICHRLDKPENLLL	148	
DB	91	YLVLVHVS	GGLFDYLVKKGRLTPKEARKFFRQIIISALDFCHSHSICHRLDKPENLLL	150	
QY	149	DERNNIRIAD	FGMASLQVDSLLTSCSGSPHYACPEVIGKEYDGRADWMSCGVILFAL	208	
DB	151	DERNNIRIAD	FGMASLQVDSLLTSCSGSPHYACPEVIRGEKYDGRKADWMSCGVILFAL	210	
QY	209	LVGALPDD	DNLRQLLEKVKRGVEHMPHFIPDCQSLLRGMIEVEPEKRLSLEIQIKHPW	268	
DB	211	LVGALPDD	DNLRQLLEKVKRGVEHMPHFIPDCQSLLRGMIEVEDAARRLTLEHIQKHIW	270	
QY	269	YLGKKEPDP	CLEPAPGRVAMRSLPSNGELDDPVLMSMASLGCGRDRERLHRLSEEE	328	
DB	271	YIGGKNEPEP	-EQPIP-RKQVIRSLPSLEDDPVLDSMHSGLGCFDRNKLQDLSSEE	328	
QY	329	NOEKMIYLL	LDKRYPCEDQDLPDRNDVDPKRKVDSPMLRHGKRPERKSMEVLS	388	
DB	329	NOEKMIYLL	LDKRYPCSEDEDDPDRNEIDPPRKVDSPMLNRHGKRPERKSMEVLS	388	
QY	389	ITDAGGSP	VPTRRALEMAQHSORSVSGASTGLSSPLSSPRSVPFSPSPGAGDE	448	
DB	389	VTD----	GGSPVPARRALEMAHQORSISGASGLSTSPSSPR-----	430	
QY	449	ARGGGSPTS	KTQLPSRGRGGAGEQPPPSARSTPLPGPGSPRSGGTPLHSLPHTP	508	
DB	431	-----	-----VTPHSPRGSPLTPKG-----TPVHTP	453	
QY	509	RASPTGTPT	TTPPPSGGVGGAAWRSRLNSIRNSFLGSPRFRHRKMQVPTAEMSSLTTP	568	
DB	454	KESPA	GTNPPTPPSSP--SVGGVPWRTRLNSIKNSFLGSPRFRHRKMQVPTPEMSNLTP	511	
QY	569	ESSPELAK	RSWFGNFI	SLDKKEQIFVLVKDKPLSSIKADIVHAFSLPSLSHSVLSQTSF	628
DB	512	ESSPELAK	RSWFGNFI	INLEKEQIFVVIKDKPLSSIKADIVHAFSLPSLSHSVLSQTSF	571
QY	629	RAEYKAS	GGPSVFQKPVRFQVDISSSEGPSPRRDGGGGGIYSVFTTILSGPSRRFKR	688	
DB	572	RAEYKATG	GPVAVQKPVKQVDITYTEGGAQKE-----NGIYSVFTTILSGPSRRFKR	625	
QY	689	VVETIOA	QLLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPGRDPELS	740	
DB	626	VVETIOA	QLLSTHDQPSAQLS-----EPPP--PAPGLS	657	
RESULT 7					
ST29 HUMAN					
ID	ST29	HUMAN	STANDARD; PRT; 736 AA.		
AC	Q81WQ3; Q60843; Q95099; Q8TB60;				
DT	10-OCT-2003	(Rel. 42, Created)			
DT	10-OCT-2003	(Rel. 42, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DE	Serine/threonine-protein kinase 29 (EC 2.7.1.37) (BRSK2) (HUSSY-12).				
GN	Name=STK29; Synonyms=PEN11B;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				

RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).	DR	EMBL; AF020089; AAD09654.1; ALT_SEQ.
RC	TISSUE=Brain;	DR	HSSP; O63450; 1A06.
RA	Guo J.H., Yu L.;	DR	Genew; HGNC:11405; STK29.
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	DR	InterPro; IPR011009; Kinase like.
RN	[2]	DR	InterPro; IPR008271; Ser_thr_pkin_AS.
RP	SEQUENCE OF 72-736 FROM N.A. (ISOFORM 2).	DR	InterPro; IPR002290; Ser_thr_pkinase.
RC	TISSUE=Brain;	DR	Pfam; PF00069; Pkinase; I.
RA	MEDLINE=21064499; PubMed=11124703;	DR	ProDom; PD000001; Prot_kinase; 1.
RX	DOI=10.1002/1097-0061(200101)18:1<69::AID-YEA647>3.3.CO;2-8;	DR	SMART; SM00220; S_TKc_1.
RA	Stanchi F., Bertocco E., Toppi S., Dioguardi R., Simonati B.,	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	DR	PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
RA	Camata N., Zimbello R., Lanfranchi G., Valle G.;	DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
RT	"Characterization of 16 novel human genes showing high similarity to	KW	Alternative splicing; ATP-binding; Serine/threonine-protein kinase;
RL	yeast sequences.";	KW	Transferase.
RN	Yeast 18:69-80(2001).	FT	DOMAIN 19 270 Protein kinase.
RP	[3]	FT	DOMAIN 424 468 Pro-rich.
RC	SEQUENCE OF 454-736 FROM N.A. (ISOFORM 2).	FT	NP_BIND 25 33 ATP (By similarity).
RA	TISSUE=Eye;	FT	BINDING 48 48 ATP (By similarity).
RX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;	FT	ACT_SITE 141 141 Proton acceptor (By similarity). EPPPPAPGL
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	FT	VARSPLIC 647 674 SWAGLGKQKVAIVYESSL (in isoform 2).
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	FT	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	FT	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,	FT	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	FT	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	FT	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	FT	
RA	Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,	FT	
RA	Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	FT	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	FT	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	FT	
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,	FT	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	FT	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	FT	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	FT	
RA	Butterfield A., Schein J.E., Jones S.J.M., Marra M.A.;	FT	
RA	Schmerch A., Schin J.E., Jones S.J.M., Marra M.A.;	FT	
RT	"Generation and initial analysis of more than 15,000 full-length human	FT	
RL	and mouse cDNA sequences.";	FT	
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	FT	
RP	[4]	FT	
RC	SEQUENCE OF 463-736 FROM N.A. (ISOFORM 3).	FT	
RA	TISSUE=Brain, and Testis;	FT	
RA	Mura K., Jinno Y.;	FT	
RL	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.	FT	
CC	-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.	FT	
CC	-1- ALTERNATIVE PRODUCTS.	FT	
CC	Event=Alternative splicing; Named isoforms=3;	FT	
CC	Name=1;	FT	
CC	isoId=Q81WQ3-1; Sequences=VSP_008154, VSP_008155;	FT	
CC	Name=2;	FT	
CC	isoId=Q81WQ3-2; Sequences=VSP_008154, VSP_008155;	FT	
CC	Name=3;	FT	
CC	isoId=Q81WQ3-3; Sequences=VSP_008156, VSP_008157;	FT	
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.	FT	
CC	-1- CAUTION: Ref.4 (AAD09654) sequence, isoform 3, differs from that	FT	
CC	shown due to a stop codon in position 663 which was translated as	FT	
CC	Gly to extend the sequence.	FT	
CC		FT	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	FT	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	FT	
CC	the European Bioinformatics Institute. There are no restrictions on its	FT	
CC	use by non-profit institutions as long as its content is in no way	FT	
CC	modified and this statement is not removed. Usage by and for commercial	FT	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	FT	
CC	or send an email to license@isb-sib.ch).	FT	
CC		FT	
DR	EMBL; AV166857; AAN87839.1; -	DR	EMBL; AV166857; AAN87839.1; -
DR	EMBL; AF533876; AAP97723.1; -	DR	EMBL; AF533876; AAP97723.1; -
DR	EMBL; AF533877; AAP97724.1; -	DR	EMBL; AF533877; AAP97724.1; -
DR	EMBL; AF533878; AAP97725.1; -	DR	EMBL; AF533878; AAP97725.1; -
DR	EMBL; AF533879; AAP97726.1; -	DR	EMBL; AF533879; AAP97726.1; -
DR	EMBL; AF533880; AAP97727.1; -	DR	EMBL; AF533880; AAP97727.1; -
DR	EMBL; AJ006701; CAA07196.1; -	DR	EMBL; AJ006701; CAA07196.1; -
DR	EMBL; BC024291; AAN24291.1; ALT_INIT.	DR	EMBL; BC024291; AAN24291.1; ALT_INIT.

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Db 571 RAEYKATGPAVFQKPVKQFQVDITYTGGEAQKE-----NGIYSVITFLLSGSPRRFKR 624
Qy 689 VVETIOAQLLSTHDQPSVQAL-----ADKXNGA 716
Db 625 VVETIOAQLLSTHDQPSVQAL-----ADKXNGA 716
Qy 717 QTRPAGAPPR-----SLOPPPG- RPDPELSSSPRGPDKK 752
Db 685 AAQAPSTPAKSAHGPLGDSAAAGPGGDAEYPTGKDTAKGPPPTARR 733

RESULT 8
Q6DMN7
ID Q6DMN7 PRELIMINARY; PRT; 653 AA.
AC Q6DMN7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Brain-selective kinase 2 (Putative serine/threonine kinase SADA
DE alpha).
GN Name=Brsk2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang W.W., Shan Y.X.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kishi M., Sanes J.R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY660739; AAT74618.1; -
DR GO; GO:0005524; P-ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR002719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 653 AA; 73149 MW; 8A23B94D71850E9A CRC64;

Query Match 58.7%; Score 2379.5; DB 2; Length 653;
Best Local Similarity 74.3%; Pred. No. 6.2e-85;
Matches 462; Conservative 53; Mismatches 42; Indels 65; Gaps 7;

Qy 89 FRYLVHVSQGGELFDYLVKKGRLTPKEARFFQIVSALDFCHSYSTCHRDLPENLL 148
Db 91 YLYLVHVSQGGELFDYLVKKGRLTPKEARFFQIVSALDFCHSHSICHRDLPENLL 150

Qy 149 DEKNRIADFGMASLQVDSLLTSCGSPHYACPEVIKGYKQGRADWMSCGVILFAL 208
Db 151 DERNRIADFGMASLQVDSLLTSCGSPHYACPEVIRGEKYGRADWMSCGVILFAL 210

Qy 209 LVGALPDDNLRQLLEKVKGVFMHPHIFPPDCQSLLRGMIEVEPKRSLQIOKHPW 268
Db 211 LVGALPDDNLRQLLEKVKGVFMHPHIFPPDCQSLLRGMIEVEPKRSLQIOKHPW 270

Qy 269 YLGKGPDPCLPAPGRVAVMSI.PSNGELDDPVLSMASLGCGRRLRLHRLSEEE 328
Db 271 YIGKGNPEP-EQPIP-RKQVIRSLPSEDIDPDVLDMSHSLGCFDRNKLQDLLSEEE 328

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Qy 329 NOEKMIYILLDRKERYPCEDQDLPPRNDVDPPKXVDSFMLSRHGRKRRPERKSMVLS 388
Db 329 NOEKMIYILLDRKERYPCEDQDLPPRNDVDPPKXVDSFMLSRHGRKRRPERKSMVLS 388
Qy 389 ITDAGGGGVPVPRRALEMAHQSRSSVSGASTGLSSSSPLSSSPRSVPFSPSPGAGDE 448
Db 389 VTD---GGSPVARRALEMAHQSRSSVSGASTGLSSPLSSPR----- 430
Qy 449 ARGGSPTSQTLPSPRGGGAGGQPPPSARSTPLPGPPGSPRSRGGTPLHSLHTP 508
Db 431 -----VTPHSPRGSPLTPKG-----TPVHTP 453
Qy 509 RASPTGTPTTPPSPGGVGGAAWRSIRNSFLGSPFRHRRKQVQVTAEMSLTP 568
Db 454 KESPAAGTPNTPPSP--SVGGVPWRTRLNSIKNSFLGSPFRHRRKQVQVTAEMSLTP 511
Qy 569 ESSPELAKRWFNGFNISLDEKBOIFVLVKDPLSSIKADIVHAFPLSPSLSHSVLSQTSF 628
Db 512 ESSPELAKRWFNGFNINLEKEQIFVVIKDKPLSSIKADIVHAFPLSPSLSHSVLSQTSF 571
Qy 629 RAEYKASGSPSVFQKPVRFQVDISSSEGPSPRRDGGGGGGIYSVTFTLISGSPRRFKR 688
Db 572 RAEYKATGPAVFQKPVKQFQVDITYTGGEAQKE-----NGIYSVITFLLSGSPRRFKR 625
Qy 689 VVETIOAQLLSTHDQPSVQALA 710
Db 626 VVETIOAQLLSTHDQPSAQLS 647

RESULT 9
Q6PHMO
ID Q6PHMO PRELIMINARY; PRT; 523 AA.
AC Q6PHMO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 4832424K13Rik protein (Fragment).
GN Name=4832424K13Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

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DR EMBL: BC056498; AAH56498.1; --
DR GO: GO:0005524; F-ATP binding; IEA.
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; P:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002290; Ser Thr pkinase.
DR InterPro: IPR008271; Ser Thr pkinase.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM0220; S_TKc; 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 523 AA; 58481 MW; 19E1AB09FF6C317D CRC64;

Query Match 54.0%; Score 2188.5; DB 2; Length 523;
Best Local Similarity 73.0%; Pred. No. 1.3e-77;
Matches 425; Conservative 51; Mismatches 41; Indels 65; Gaps 7;

QY 129 DFCYSYICHRDLKPENLLLDKNNIRIADFGMASLQVDSLLTSCGSPHYACPEVIK 188
Db 1 DFCSHSICHRDLKPENLLLDKNNIRIADFGMASLQVDSLLTSCGSPHYACPEVIR 60

QY 189 EKYDGRADMMSCGVILFALLVGLPDDDDNLRLQLLEKVRGVFHMHPHFPDPCOSILRG 248
Db 61 EKYDGRKADVMSCGVILFALLVGLPDDDDNLRLQLLEKVRGVFHMHPHFPDPCOSILRG 120

QY 249 MIEVEPEKRLSEIQKHPWYLGKHGHPDPCLEAPGRVAMRSLPNSGELDPDLVESMA 308
Db 121 MIEVDAARLTLEHFKQHWIIGGKNEPEP-EQIP-RKQVIRSLPSLEDIDPDVDSMH 178

QY 309 SLGCFRDRRLHRELRSEENQEKMYLLLDKRYPCSDQDLPANDVDPKPKVDS 368
Db 179 SLGCFRDRNKLQDLSEENQEKMYLLLDKRYPCSDQDLPANDVDPKPKVDS 238

QY 369 PMLSHRGKRRPKRMEVLSTIDAGGSGVPVTRALMAHQSRKSVSGASTGLSSSP 428
Db 239 PMLNRHGRKRRPKRMEVLSTVD---GGSPVPAARAIEAQAHQSRKSVSGASTGLSTSP 295

QY 429 LGSRSRPFVFSFEPGAGDEARGGSPSTKTQTLPSRPGGAGQEPSPASSTPLPG 488
Db 296 LGSRP-----VTFHPSRPGSPPLPT 314

QY 489 PGSPRSSGTLPHSLHTPRASPTCTPTPPSPGGVGGAWRSLNIRNSFLGSP 548
Db 315 PKG-----TPVHTPKESPAGTNPPTPPSP--SVGGVPWRTLNLSIKNSFLGSP 361

QY 549 RHRRKQVPTAEMLSPSPESPELAKRSWFGNFISLDKKEQIFLVLDKXPLSSIKADI 608
Db 362 RHRRKQVPTAEMLSPSPESPELAKRSWFGNFINLEKEQIFVWIKDXPLSSIKADI 421

QY 609 VHAFSLPSLSHVLSTQSFRAEYKASGSPVQKPVRFQVNDISSEGEPPSPRDGSGG 668
Db 422 VHAFSLPSLSHVSISQTSFRAEYKATGTPAVFQKPVFQVDITYTTEGEAQKE----- 475

QY 669 GGIYSVTFTLISGSPRRFKRVVTIOALLSTHDQPSVQALA 710
Db 476 NGIYSVTFTLISGSPRRFKRVVTIOALLSTHDQPSAQHLS 517

RESULT 10
Q9VUV4 ID Q9VUV4 PRELIMINARY; PRT; 861 AA.
AC Q9VUV4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG6114-PA.
GN ORFNames=CG6114;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;


```

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN (5)
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN (6)
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AE003529; AAF49569.3; -.
DR HSSP; P49137; INKK.
DR FlyBase; FBgn0036544; CG6114.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR008271; Ser_Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase,
SQ SEQUENCE 861 AA; 95526 MW; CA9E86B2B4A7BB37 CRC64;

Query Match 39.2%; Score 1588; DB 2; Length 861;
Best Local Similarity 50.1%; Pred. No. 3.8e-54;
Matches 347; Conservative 91; Mismatches 143; Indels 112; Gaps 22;

QY 89 FRVLVLESHVSGGELFDYLVKKGRITPKKARKFFRQIVSALDFCHSYSTRDLKPNLL 148
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
89 YLYLVLESHVSGGELFDYLVKKGRITPKKARKFFRQIVSALDFCHSHSICHDLKPNLL 148

QY 149 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIRGEKYGRRADWMSGCVILYAL 208
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
149 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIRGEKYGRRADWMSGCVILYAL 208

QY 209 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCOSLLRGMIEVEPEKRLSLEQIQHPW 268
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
209 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCOSLLRGMIEVEPEKRLSLEQIQHPW 268

QY 269 Y-LGKHEPD---FCLPAPGPRVAMRSLPNSGLDPPVLESMSLGCFFRDRELRHLR 324
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
269 VTAGGGELELELPMVEV-----VQTHVPIPTATAVDPDLNALICSLGCFKEKLIQELL 323

QY 325 SEENQEKMIYLLLDKERYPSCEDOD---LPPND---VDPKRVDSPLSRHGKRR 378
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
324 SSSHTKVIYVLLERKRRPALEDDDEIAQKRSSELDVDPKRLDTCRI--NGTNA 381

QY 379 PERKSMEVLSITDAGGGSVPV-PTTRALEM-----AQHSQRS-----RSVSGASTG 423
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
382 PSYQGI-----SEGSLPTPRQAFNFRSYSTRNHQRSPVTTVTSVRSSSYHSPT 432

QY 424 LSSGPLS-----PRSPV-----FSPSPG-----AGD--- 447
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
433 RCNPFMSAQQAQANAI RPSPPAAGRTHSTYGD RSGHSSVSRTPSHSSQKIEGDV 492

QY 448 -----EARGGSGPTSKQT-LPSRGRGGGAGCEQPPPPSARSTPLPGPGGS 492
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
493 VREPRIERRSLRQERGGSPDRDGCIPGSPGNGSGSGTSASPSVHHRANSGP--- 549

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QY 269 Y-LGGKHEPD---PCLEPAPGRVAMRSLPSNGELDPDVLMSASLGCFPRDRERLHRLR 324
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 257 VTAGGKELELPMMEV-----VQTHVTPNASAVDTDLNAICSLGCFKEKLIQELL 311
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 325 SEENQKMYIYLLDKERYPCEDQD--LPRNDV----DPPRKRVDSPLSRHGRKR 378
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 312 SPHNTEKVIYFLLDKRRRPAIEDEEDVLRPNNDIIEIADPPKRLDTCRIN----- 365
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 379 PERKMEVLSITDAGGSGSPVPTTRALEMAHQSORSRVSGASTGLSSPLSPSPSPVPS 438
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 366 -GSSLSYGQISE-----GSLTSRRQTFNNGHRSHSGTSG---GSRKSPSSVPLSRSSY 417
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 439 FSPFPGADGARGGSGSTQTLPSRGPGGAG-----EQPPPSARSTPLP 487
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 418 QSPTRGV---VWNSSQSLKSFSDVPR-----DFGRTLVLFLLDQLDPLPSSPNAASNR 469
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 488 GPPGSPRSS-----GGTPLHSPHTPRASPTGTGP-----TTPPSPG 526
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 470 HSNYSRPSSTKSVIDSSPVH---HRANGPAVTGVLFSSETDSNNMTSSINAI PGSPIL 526
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 527 G-----VGGAAWRSLNSINSLGSPRHRHRRKQVPTAEWSSSLTPSPPELAKR 577
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 527 GSPQOLQAVTTGSQLWKTLTNKNSFLGSPKFRHRRKQISTEE--VHLTPSSPELTCK 584
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 578 SWFNFTSLDKERQIFVLKDKPLSSIKADIVHAFSLPSLSHSLVLSOTSFRAEYKASG- 636
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 585 SWFNGLMTTEKDETFTVLVKGKPLATVKAHLIHAFLSWELSHSLVSPMFRVYKGGT 644
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 637 GPSVQKVRPQVDITSSSEGPSPRRDGGGGGIYSVFTLISGSPRRKRVVETIOA 695
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 645 GPTMFQHRVIRQVDINTI-----CKQGDVGDMLFAITFTLISGNIRRRFRICEHTQA 696
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 12

O61298 PRELIMINARY; PRT; 698 AA.
 ID O61298;
 AC O61298;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE HrPOPK-1 protein.
 GN Name=HrPOPK-1;
 OS Halocynthia roretzi (sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyuridae; Halocynthia.
 OX NCBI_TaxID=7729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Egg;
 RX MEDLINE=98440280; PubMed=9767157; DOI=10.1016/S0925-4773(98)00100-2;
 RA Sasakura Y., Ogasawara M., Makabe K.W.;
 RT "Naturally localized RNA encoding a serine/threonine protein kinase
 in the ascidian, Halocynthia roretzi.";
 RL Mech. Dev. 76:161-163(1998).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AB014885; BAA28663.1; --
 DR HSP; Q63450; IAO6
 DR GO; GO:000524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr pkinase.
 DR InterPro; IPR008271; Ser Thr pkin_ AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOW; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 698 AA; 78607 MW; B29B1751E83200BF CRC64;
 SQ

RESULT 13

Q19469 PRELIMINARY; PRT; 914 AA.
 ID Q19469;
 AC Q19469; Q9BMN6;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein F15A2.6 (Serine/threonine kinase SAD-1).
 GN Name=sad-1; ORFNames=F15A2.6;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2; PubMed=9851916;
 RX MEDLINE=99069613; PubMed=9851916;
 RT none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.

Query Match 35.5%; Score 1438; DB 2; Length 698;
 Best Local Similarity 48.4%; Pred. No. 2e-48;
 Matches 312; Conservative 103; Mismatches 112; Indels 118; Gaps 21;
 QY 89 FRYLVLEHVSGLFDLYLVKGRITPKAEKFRQIVSALDFCHSVSICHRLDKPENLLL 148
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 85 YLYLLEHVSGLFDLYLVKGRITPKAEKFRQIVSALDFCHSVSICHRLDKPENLLL 144
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 149 DEKNIRIADFGMASLOVGDLSLETSCGSPHYACPEVIKGEKYDGRADWMSGCVILFAL 208
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 145 DEKNIKVADFGMASLOVGDLSLETSCGSPHYACPEVIRGERYDGTADWMSGCVILFAL 204
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 209 LVGALPDDDLNRLLEKVRGVFHMHPFPDCCQSLRGMIEVEPKRLSLEIOIOPW 268
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 205 LVGALPDDDLNRLLEKVRGVYHIPIHVPDPAQNLRLGMIDVPPDKRLSQQVLOQHPW 264
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 269 YLGGKHE-----PD---PCLEPAPGRVAMRSLPSNGELDPDVLMSASLGCFPRDRER 318
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 265 MRPGSNSVEGLVTPDPVFPVIDCV-----LPESVDPDVLASMTSLGCFCKNEK 316
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 319 LHRELRSBEENQEKMYIYLLDKERYPCEDQ--DLPNDVDPKRYD--SPMLSRHG 375
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 317 LLKNLITEEQNTEKVVYMLRRKKRYPDFDDADSLPCKHPDAPRKRVDTSTSSSNG 376
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 376 -----KRRPERK-SNEVLSITDAGGSGSPVPTTRALEMAHQSORSRVSGASTGLSSPL 429
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 377 DDWCNVNIPQRKMSAESLCLTDS-----SSPLLRSK--KSTETHQRSQSL-----TGESNSRL 427
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 430 SSPRSVPSFSPGAGDEARGGSGSTQTLPSRPGGAGQPPPPPPPPPPPPPPPPPPPP 489
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 428 -----VCNISQTKAESKSRINGTPVRGTTCS-----NQVP----- 461
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 490 PGSPRSSGTPPLHSPHTPRASPTGTPTTTPPSPGGVGAWSRLNSINSLSPSS 549
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 462 -----QINTPAS-----PNP-----WQRLASLKNTPGSGPR 488
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 550 FHRKMQVPTAEWSSSLTPSPPELAKRSWFGNFIQLD-----KEQIFVLKDKPLS 602
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 489 FHRKMQVPTAEWSSSLTPSPPELAKRSWFGNFIQLD-----KEQIFVLKDKPLS 547
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 603 SIKADIVHAFSLPSLSHSLVLSOTSFRAEYKASG--GPSVF-QKPVRFQVDI-----S 652
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 QY 548 SVKSELVHAFSLPSLSHSLVLSOTSFRAEYKASG--GPSVF-QKPVRFQVDI-----S 607
 Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

Db 285 ANAISRPSAPACRTHSTYGDRLDRSGHSSVSRTPSHSSQKSTEGDVVVVREPRIERRDS 344

Qy 448 --EARGGSGTSTKTQ--LPSRGRPGGACGQPPPSARSTPLPGPGSPRSSGGTTLHSP 504

Db 345 LRQERGGSGPRDGDGCGIPPGSGNSGSGTSAPSVMHRANGP-----TIAISWFHDP 399

Qy 505 LHTPRASPTGTP--GTPP--PPSPGGVGGAARSLRSLRNSIRNSFLSGSPRFRHRKMQVPT 559

Db 400 DSNVSNVNPNGSPMNNSSPMPGSPCNTPGQLWKRLTNIKNSFLGSPRFRHRKMQV-S 458

Qy 560 AEEMSSITPSSPELAKRSGWFGNFIQLDKEEQIFLVKOKPLSSIKADIIVHAFSLSPSL 619

Db 459 ADEV-HLTPSSPELTKRSWFGNFIQLDKEEQIFLVKOKPLSSIKADIIVHAFSLMAELS 517

Qy 620 HSVLSQTSFRAEYKASG-GPSVFQKPVRFQVDLSSSEGGPPSPRRDGGSGGGIYSVTFTL 678

Db 518 HSVVSPTSFVEYKRNNGPVMFQRHVQFQVDISAI-----CKQGDIAFMLFAUTFTL 570

Qy 679 ISGSPRRFRKRWETIOAQLLS 699

Db 571 LSGNIRFRACEHIQSVCS 591

RESULT 15

Q6C6T2 PRELIMINARY; PRT; 1058 AA.

AC Q6C6T2

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Similar to sp|P34244 Saccharomyces cerevisiae YKL101w HSL1 ser/thr protein kinase.

DE ORFNames=YAL10E06523g;

OS Yarrowia lipolytica CLIB99.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Dipodascaceae; Yarrowia.

OX NCBI_TaxID=284591;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CLIB99;

RG Genolevures;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boismare A., Boyer J., Cattolico L., Confanioli F., de Daruvar A., Despons E., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.L.;

RT "Genome evolution in yeasts.";

RL Nature 430:35-44(2004).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CLIB99;

RA Genoscope;

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL; CR392131; CAG79212.1; -

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR InterPro; IPR008271; Ser_thr_kinase.

DR InterPro; IPR001245; Tyr_kinase.

DR Pfam; PF00069; Kinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TK; 1.

DR SMART; SM00219; TyKc; 1.

DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 1058 AA; 117047 MW; D999B29BC20B8AC0 CRC64;

Query Match 18.0%; Score 731; DB 2; Length 1058;

Best Local Similarity 26.5%; Pred. No. 7, 4e-21;

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Qy 147 LLDEKNIRIADFGASLQVGSLSLETSCGSHYACPEVKGKGYDKGRADWMSQGVILF 206

Db 61 LLDKNRNIXIADFGMAALET-DRMLETSCGSHYASPEIVAGKTYHGAPSDIWSGCIILF 119

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Db 237 LSPDANPEKTFYCLLMKRYRHHAAVAATPPTLQOOQOEQMPAMHKSHSSRKHQR 296

Qy 378 RPERKMEVLISITDAGGGSPVPTFRA-----LEMAQHSQRS-RSVSGASTG----- 423

Db 297 KTSNHSRL-----GSRGLSVSVSAHKRGVSFTVKKRSQOSIRSMGSAASNVASVP 350

Qy 424 ---LSSSLSSPRSPV-----FSFSPGAGDEARGGSGTSTKTQTLPSRGRGGGAGEQ 475

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Qy 498 -GTPLHS-----PLHTPRASPTGTPTGTT----- 525

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Qy 526 GGVGGGAWR----- 538

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Db 787 HQOQQOQO-----HQLQAPVPFREKPVVSAPRRPAP 818

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
13019.891 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
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7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	723.6	31.6	881	5	BQ717903	BQ717903 AGNCOURT
3	671	29.3	671	7	CN365650	CN365650 170005325
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5	653.2	28.5	831	2	BF529743	BF529743 602044002
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7	602.2	26.3	658	4	BG818795	BG818795 602781839
8	601.8	26.3	693	6	CB056707	CB056707 NISC fj19
9	600	26.2	770	7	CV056702	CV056702 AGNCOURT
10	595.8	26.0	615	7	CV023843	CV023843 878 Full
11	592.4	25.9	698	5	BN948524	BN948524 UI-M-EGOP
12	579.8	25.3	693	7	CO393904	CO393904 AGNCOURT
13	574.8	25.1	742	5	BN944329	BN944329 UI-M-EHOP
14	571.4	25.0	686	6	CA319620	CA319620 UI-M-FWO-
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16	556	24.3	556	7	CK819107	CK819107 IF08a12.Y
17	548.6	24.0	840	7	CO400752	CO400752 AGNCOURT
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22	540.4	23.6	658	5	BQ573641	BQ573641 UI-M-FDO-
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ALIGNMENTS

RESULT 1
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LOCUS Homo sapiens mRNA; cDNA DKFZp547E1613 (from clone DKFZp547E1613).
DEFINITION
ACCESSION AL834275.1 GI:21739846
VERSION
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2720)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
CONSRM The German cDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Dueseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp547E1613) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp547E1613 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
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ORIGIN

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230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@eron.com
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FEATURES
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QY 1123 GGAAGCGCG 1133
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Db 661 GGAAGCGCG 671
|||||

LOCUS BUS20742 950 bp mRNA linear EST 12-SEP-2002
DEFINITION AGENCOURT_10153453 NIH_MGC_134 Mus musculus cDNA clone
IMAGE:6518740 5', mRNA sequence.
ACCESSION BUS20742
VERSION BUS20742.1 GI:22828268
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 950)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14100 row: p column: 05
High quality sequence stop: 714.
Location/Qualifiers
1. .950
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6518740"
/issue_type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 134"
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 Kb. Constructed by Resgen, Invitrogen Corp. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 28.7%; Score 657; DB 5; Length 950;
Best Local Similarity 89.6%; Pred. No. 3.1e-142;
Matches 763; Conservative 0; Mismatches 81; Indels 8; Gaps 5;

QY 1352 GCGGGGGCTCCCGACTTCCAAACGACAGCGTGCCTTCTCGGGGCCCGAGGGTGGG 1411
|||||
Db 1 GCGGGGGCTCCCGACTTCCAAACGACAGCGTGCCTTCTCGGGGCCCGAGGGTGGG 59
|||||
QY 1412 GCGCGGGGAGAGCGCCCGCCCGCCAGTGCCTCCACACCCCTGCCCGGCCCGCCAG 1471
|||||
Db 60 GCGCTGGAGAGCAGCCACCCCGCCAGTGCCTCCACGCGCTTGCCTGGACCCAG 119
|||||
QY 1472 GCTCCCGCGCTCTCTGGGGGACCCCTTGCACCTGCCTCTGCACAGCCCGCGGCCA 1531
|||||
Db 120 GCTCCCGCGCTCTCTGGGGGACCCCTTGCACCTGCCTCTGCACAGCCCTCGAGCCA 179
|||||
QY 1532 GTCCCAACCGGGGACCCCGGGGACAAACACCCCGCCCGCGCGGTGGCGTGGGGGAG 1591
|||||
Db 180 GCGCTAGGGGACCCCGAGAACGAGCGCCACCTCCAGCCCGAGCGGTGGCGTGGGGGAG 239
|||||
QY 1592 CGCGCTGGAGAGTGTCTCACTCATCGGAAAGCTTCTTGGGGTCCCGCTCGCTTC 1651
|||||
Db 240 CGCGCTGGAGAGTGTCTCACTCATCGGAAAGCTTCTTGGGGTCCCGCTCGCTTC 299
|||||
QY 1652 ACCGGCGCAGAGTGCAGGTCCCTTACCGCTGAGGAGATGTCACGCTTGACCGAGAGTCCT 1711
|||||
Db 300 ACCGGCGCAGAGTGCAGGTCCCTTACCGCGCAGGAGATGTCACGCTTGACCGAGATCCT 359
|||||
QY 1712 CCCCGGAGCTGGCAAAACGCTCCTGCTTGGGAACTTCATCTCTTGGACAAAGAAC 1771
|||||
Db 360 CTCTGAGCTGGCAAAACGCTCCTGCTTGGGAACTTCATCTCTTGGACAAAGAAC 419
|||||
QY 1772 AATATTTCTCTGCTGTAAGGACAAACCTCTCAGCAGCATCAAGACGACATCGTCCATG 1831
|||||

RESULT 4
BUS20742

Db	420	AAATATTCTCTGCTAAAGGACAAACCTCTCAGCAGCATCAAAGCGGACATTGTCCATG	479
Qy	1832	CCTTTCTGTGATCCCGAGCCTGAGTCACAGTGTGCTCACAGCAGCTTCAGGGCCG	1891
Db	480	CCTTTCTGTGATCCCGAGCCTGAGTCACAGTGTACTGTACAGCAGCTTCAGGGCCG	539
Qy	1892	AGTACAAGGCGAGTGGGGCCCCCTCCGTCTTTCAAAAAGCCGTCGCTTCCAGTGGACA	1951
Db	540	AATACAAGGCCAGCGGGCCCCCTCCGTCTTTCAGAAGCCGTGTCGGCTTTCAGGTGACA	599
Qy	1952	TCAGCTCCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGTGGCGCA	2011
Db	600	TCAGCTCCTCTGAGGGTCCAGAACCCTCACCCCGAAGAGATGGCAGCAGTGGAGGTGGCA	659
Qy	2012	TCTACTCCGTCAACCTTCACCTCTCATCTCGGGTCCCGAGCGCTCGGTTCAAGCGAGTGTGG	2071
Db	660	TCTACTCAGTCAACCTTTTACTCTCATCTCCGGTCCCGAGCCGTCGGTTCAAAAGTGTGTAG	719
Qy	2072	AGACCATCCAGGCACAGTCTCTGAGCACTCATGACCAG-CCTCCGTGCAGGCCCT--GGC	2129
Db	720	AGACCATCCAGGCACAGTTGCTGAGTACTCAGGACAGCCCTCCGTGCAGGCCCTTGGGC	779
Qy	2130	AGACGAGAAGAACGGGGCCACAGA---CCCGGCTGTGTTGGT--CCCAACCCCGAAGCCTG	2184
Db	780	AGATGAGAAGAACGGAGCCCCAGACCCGGGSCCTGCTGGGACCCCAACCCCGAAGCCTG	839
Qy	2185	CAGCCCCCAACC	2196
Db	840	CAGCCCCCAACC	851

RESULT	5
LOCUS	BFS29743
DEFINITION	BFS29743 831 bp mRNA linear EST 11-DEC-2000 602044002P1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181688
ACCESSION	BFS29743
VERSION	BFS29743
KEYWORDS	BFS29743.1 GI:11617106
SOURCE	EST.
ORGANISM	Homo sapiens (human) Homo sapiens Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 831)
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ .
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	

FEATURES
source

RESULT 6	ACCESSION	REFERENCE
CA984329	VERSION	AUTHORS
LOCUS	KEYWORDS	
DEFINITION	SOURCE	
	ORGANISM	

ORIGIN	Query Match Best Local Similarity Matches 711, Conservative 0; Mismatches 23; Indels 4; Gaps 4;	28.5%; Score 653.2; DB 2; Length 831; Pred. No. 2.4e-141;
Qy	268 AGGTACTGTGTTTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTTAAAGAAG	327
Db	42 AGGTACTGTGTTTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTTAAAGAAG	101
Qy	328 GGGAGACTGAGCCCAA - GGAGGCCCAAGTTCCTTCGGCCAGATTGTGTGCGCTGGA	386
Db	102 GGGAGACTGAGCCCAAAGGGAGGCCCAAGTTCCTTCGGCCAG - TGTGTTCGCGCTGGA	160
Qy	387 CTTCTGCCACAGCTACTCCATCTGCCACAGAGACTTAAAGCCCGAGAACCTGCTTTTGGGA	446
Db	161 CTTCTGCCACAGCTACTCCATCTGCCACAGAGACTTAAAGCCCGAGAACCTGCTTTTGGGA	220
Qy	447 TGAGAAAAACAATCCGCATTTGCAGACTTCGGCATGCGCGTCCCTGCAGGTGGGGGACAG	506
Db	221 TGAGAAAAACAATCCGCATTTGCAGACTTCGGCATGCGCGTCCCTGCAGGTGGGGGACAG	280
Qy	507 CTTCTGGAGACAGCTGCGGGTCCCCCAATTATGCGTGTCCAGAGTGATTAAAGGGGGA	566
Db	281 CTTCTGGAGACAGCTGCGGGTCCCCCAATTATGCGTGTCCAGAGTGATTAAAGGGGGA	340
Qy	567 AATAATATGATGGCGCGCGGACAGATGTGGAGCTGTGGAGTCAATCTTCGCGCCCTGCT	626
Db	341 AATAATATGATGGCGCGCGGACAGATGTGGAGTCAATCTTCGCGCCCTGCT	400
Qy	627 CGTGGGGGCTCTGCGCTTTGATGACGACAACTCCGCGCAGCTGCTGGAGAGGTGAAACG	686
Db	401 CGTGGGGGCTCTGCGCTTTGATGACGACAACTCCGCGCAGCTGCTGGAGAGGTGAAACG	460
Qy	687 GGGCGTCTTCCACATGCCCACTTCATTCCTCCAGATTGCCAGAGCTCTCTGAGGGGAAT	746
Db	461 GGGCGTCTTCCACATGCCCACTTCATTCCTCCAGATTGCCAGAGCTCTCTGAGGGGAAT	520
Qy	747 GATCGAAGTGGAGCCGCAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTCTGGTA	806
Db	521 GATCGAAGTGGAGCCGCAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTCTGGTA	580
Qy	807 CCTAGGCGGGAAACACGAGCCAGACCCGTCGCTGGAGCCAGCCCTGCGCCCGGGTAGC	866
Db	581 CCTAGGCGGGAAACACGAGCCAGACCCGTCGCTGGAGCCAGCCCTGCGCCCGGGTAGC	640
Qy	867 CATGCGG - AGCTCTGCCATCCAAACGAGAGCTGGACCCCGACGCTCTTAGAGAGCATGGCAT	925
Db	641 CATGCGGAGCCTGSCCATCCAAACGAGAGCTGGA - CCGAGCGTCTTAGAGAGCATGGCAT	699
Qy	926 CACTGGGCTGTTTCAGGGACCGGAGAGGCTGCATTCGCGAGCTCGGCAGTGAGGAGGAGA	985
Db	700 CACTGGGCTGTTTCAGGGACCGGAGAGGCTGCATTCGCGAGCTCGGCAGTGAGGAGGAGGA	759
Qy	986 ACCAAGAAAAGATGATAT 1003	
Db	760 CCACAAAATGGTTTATAT 777	
RESULT 6		
CA984329		
LOCUS	CA984329	868 bp mRNA linear EST 06-JAN-2003
DEFINITION	AGENCOURT 11296377 NIH MGC 164 Mus musculus cDNA clone	
	IMAGE:30147920 5', mRNA sequence.	

RESULT 6	CA984329	868 bp	linear	EST 06-JAN-2003
LOCUS	CA984329			
DEFINITION	AGENCOURT_11296377 NIH_MGC_164 Mus musculus cDNA clone			
	IMAGE:30147920 5', mRNA sequence.			
ACCESSION	CA984329			
VERSION	CA984329.1	GI:27516985		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 868)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDA0065 row: p column: 09
High quality sequence start: 15
High quality sequence stop: 649.
Location/Qualifiers
1. .868
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30147920"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 164"
/note="vector: PCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;
Non-normalized full-length enriched library from pooled
mouse embryonic limb, maxilla and mandible, day 10.5 and
11.5 (size selected for the 0.5-1 kb fragments) Cloned
directionally, priming method: Oligo-dT. cDNA enrichment:
>1k bp, Average insert size 1.8k bp. Priming sequence:
5'-GACTAGTCTTGTAGATCGAGCGCGCCCT(T) 3'. Tissue contributed
by, David Rowe. Library constructed by ResGen, Invitrogen
Corp."

FEATURES
source
1. .868
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30147920"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 164"
/note="vector: PCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;
Non-normalized full-length enriched library from pooled
mouse embryonic limb, maxilla and mandible, day 10.5 and
11.5 (size selected for the 0.5-1 kb fragments) Cloned
directionally, priming method: Oligo-dT. cDNA enrichment:
>1k bp, Average insert size 1.8k bp. Priming sequence:
5'-GACTAGTCTTGTAGATCGAGCGCGCCCT(T) 3'. Tissue contributed
by, David Rowe. Library constructed by ResGen, Invitrogen
Corp."

ORIGIN
Query Match 28.5%; Score 652; DB 6; Length 868;
Best Local Similarity 92.0%; Pred. No. 4.5e-141;
Matches 710; Conservative 0; Mismatches 60; Indels 2; Gaps 2;
QY 1215 GGAGATGCCAGACAGCAGACAGATCCGTCAGTGGAGCTCCAGGCTCCAGGCTCTGTC 1274
Db 1 GGAGATGCCAGACAGATCCAGATCCGTCAGTGGAGCTCCAGGCTCCAGGCTCTGTC 60
QY 1275 CTCAGGCTCTTAAGACAGCCCAAGAGTCCGGTCTTTCTTTTTCACGGAGCGGGGC 1334
Db 61 CTCAGGCTCTGAGCAGCCCAAGAGTCCGGTCTTTCTTTTTCACGGAGCGGC 120
QY 1335 TGGAGATGAGCTCGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTTCG 1394
Db 121 TGGAGATGAGCTAGAGCGGAGGCTCCCAACTTCCAAACGAGAGCTGCTTCG 180
QY 1395 GGGCCCCAGGGTGGGGGCGCGGGAGCAGCCCCCGCCAGTGCCCGCTCCACACC 1454
Db 181 GGGCCCCAGAGGTGGGGGCGCTGGAGAGCAGCCACACCCCCAGTGCCTCCAGCC 240
QY 1455 CTTGCCCGCCCCCAGAGCTCCCGCTCTCTTGGCGGGAGCCCGCTTGACTGCTCT 1514
Db 241 CTTGCTGGACACACAGGCTCCCGCTCTCTTGGCGGGAGCCCGCTTGACTGCTCT 300
QY 1515 GCACAGCCCCGGGCGAGTCCACCGGACCCCGGGGACACACACCCCCCAGCCCGG 1574
Db 301 GCACAGCGCTCGAGCGAGCCCTTACGGGACCCCGAGAGCAGCCACCTCCAGCCAG 360
QY 1575 CGGTGGCTCGGGGAGCGCTCGAGGAGTGTCTCAACTCCATCCGCAACAGTTCT 1634
Db 361 CGGTGGCTCGGGGAGCGCTCGAGGAGTGTCTCAACTCCATCCGCAACAGTTCT 420
QY 1635 GGGCTCCCTCTCTTCCAGCGGCGAGATGAGTCCCTACCGCTGAGGAGTGTCCAG 1694
Db 421 GGGCTCCCTCTCTTCCAGCGGCGAGATGAGTCCCTACCGCTGAGGAGTGTCCAG 480
QY 1695 CTTGAGCGCAGAGTCTCTCCCGGAGCTGGCAAAACGCTCTGTTTCGGGAATTCATCTC 1754
Db 481 TTTGACACCAAGATCTCTCTGAGCTGGCAAAACGCTCTGTTTCGGGAATTCATCTC 540

QY 1755 CTTGACAAAGAGAAACAAATATTTCTCGTAAAGGACAAACCTCTCAGCAGCATCA 1814
Db 541 CTTGACAAAGAGAAACAAATATTTCTCGTAAAGGACAAACCTCTCAGCAGCATCA 600
QY 1815 ACCAGACATCGTCCATGCTTTCTGTCATCCCGAGCTGAGTACAGTGTCTGTCA 1874
Db 601 AGCGGACATTTGTCATGCTTTCTGTCATCCCGAGCTGAGTACAGTGTCTGTCA 660
QY 1875 GACCAGCTTCAGGCGCGAGTACAAGCCAGTGGCGG-CCCTTCCTGTTTCCAAAGCCG 1933
Db 661 GACCAGCTTCAGGCGCGATACAAAGCCAGCGCGGCCCTCCGTTCTTCCAGAGCTG 720
QY 1934 TCCGTTCCAGTGGACATCAGCTCC-TCTGAGGTCCAGAGCCCTCCCGC 1984
Db 721 TCCGTTTTCAGTGGACATCAGCTCC-TCTGAGGTCCAGAGCCCTCCCGC 772

RESULT 7
BG819795 658 bp mRNA linear EST 22-MAY-2001
LOCUS 602781839F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4932680
DEFINITION 5', mRNA sequence.
ACCESSION BG819795 1 GI:14167382
VERSION BG819795
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 658)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0858 row: n column: 09
High quality sequence stop: 612.
Location/Qualifiers
1. .658
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4932680"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_Brn67"
/notes="Organ: brain; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 26.3%; Score 602.2; DB 4; Length 658;
Best Local Similarity 98.4%; Pred. No. 1.8e-129;
Matches 619; Conservative 0; Mismatches 8; Indels 2; Gaps 1;
QY 811 GCGGGGAAACACGAGCCAGACCCGCTGCTGAGCAGCCCTGCGCCCGGTAGCCATG 870
Db 1 GCGGGGAAACACGAGCCAGACCCGCTGCTGAGCAGCCCTGCGCCCGGTAGCCATG 60
QY 871 CGGAGCTTCCATCCACGCGAGCTGAGCCCGACCTCTAGAGAGCATGGCATCACTG 930
Db 61 CGGAGCTTCCATCCACGCGAGAGCTGAGCCCGACCTCTTAGAGAGCATGGCATCACTG 120
QY 931 GGCTGCTTCCGGGACCGGAGAGGCTGCATCGGAGCTGCGAGTGGAGGAGGAGCAACAA 990

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Db 121 GCTGCTTCAGGACCGGAGAGGCTGCATCGCAGCTGCGCATGAGGAGGACCA 180
Qy 991 GAAAGATGATATATTATCTGCTTTTGATCGGAAGAGCGGTATCCAGCTGTGAGGAC 1050
Db 181 GAAAGATGATATATTATCTGCTTTTGATCGGAAGAGCGGTATCCAGCTGTGAGGAC 240
Qy 1051 CAGGACCTGCTCCCGGATGATTTGACCCCGGAGCGGTGATGATTTCCCATG 1110
Db 241 CAGGACCTGCTCCCGGATGATTTGACCCCGGAGCGGTGATTTCCCATG 300
Qy 1111 CTGAGCCGCTCACGGGAAGCGGACGAGGCGGAAGTCCATGGAAGTCCCTGAGCATCAC 1170
Db 301 CTGAGCCGCTCACGGGAAGCGGACGAGGCGGAAGTCCATGGAAGTCCCTGAGCATCAC 360
Qy 1171 GATCCCGGGGTGTGCTCCCTGTATCCACCGGCGGCTTTGGAGATGGCCCGACAC 1230
Db 361 GATCCCGGGGTGTGCTCCCTGTATCCACCGGCGGCTTTGGAGATGGCCCGACAC 420
Qy 1231 AGCCAGAGATCCCTAGGCTCAGTGGAGCTTCCAGGGTCTGTCTCAGGCCCTTAAGC 1290
Db 421 AGCCAGAGATCCCTAGGCTCAGTGGAGCTTCCAGGGTCTGTCTCAGGCCCTTAAGC 480
Qy 1291 AGCCAGAGATCCCTAGGCTCAGTGGAGCTTCCAGGGTCTGTCTCAGGCCCTTAAGC 1350
Db 481 AGCCAGAGATCCCTAGGCTCAGTGGAGCTTCCAGGGTCTGTCTCAGGCCCTTAAGC 540
Qy 1351 GCGCGGGGCTCCCGACTTCCAAACGCGAGCTGCTTCCGGGGCCCCAGGGGTGGG 1410
Db 541 GCGCGGGGCTCCCGACTTCCAAACGCGAGCTGCTTCCGGGGCCCCAGGGGTGGG 598
Qy 1411 GCGCGGGGAGAGAGCCCCCGCCCCCAG 1439
Db 599 GCGCGGGGAGAGAGCCCCCGCCCCCAG 627
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RESULT 8

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CB056707
LOCUS NISC_j19g03.w1 Soares NMBP13-15 Mus musculus cdna clone EST 17-JAN-2003
DEFINITION IMAGE:4848580 5', mRNA sequence.
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```
CB056707
VERSION CB056707.1 GI:27794994
```

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KEYWORDS EST.
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SOURCE Mus musculus (house mouse)
```

```
ORGANISM Mus musculus
```

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REFERENCE 1 (bases 1 to 693)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
JOURNAL NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
```

```
CONTACT: Robert Straubeberg, Ph.D.
Email: cgaps-remail.nih.gov
```

```
CDNA Library Preparation:
DNA Sequencing by: The I.M.A.G.E. Consortium/LLNL
```

```
Sequencing Center (NISC)
Clone distribution: NCI-CCAP clone distribution information can be
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found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
```

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Plate: LLAM10779 row: N column: 5
Seq primer: T7 primer.
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FEATURES
Location/Qualifiers
1..693
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/organism="Mus musculus"
/mol_type="mRNA"
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/clone="IMAGE:4848580"
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/tissue_type="pituitary gland"
/dev_stage="juvenile, 13-15 days"
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/lab_host="DH10B (phage-resistant)"
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/clone_lib="Soares NMBP13-15"
/notes="Organ: Brain; Vector: pT7T3D-PacI; Site_1: NotI;
Site_2: EcoRI; 1st strand cdna was primed with a NotI-
oligo(dT) primer
5'-AAGTGAAGAATTCCGGCGCGCTGACCATGATGTTTTTTTTTTTTTTT-3';
double-stranded cdna was ligated to EcoRI adaptor
5'-AATTCGGACGAGG-3' and 5'-CTCGTGGCG-3' (Pharmacia),
digested with NotI and cloned into the NotI and EcoRI
sites of the pT7T3D-PacI vector. Library went through one
round of normalization, and was constructed in the
laboratory of M. Bento Soares (University of Iowa)."
```

ORIGIN

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Query Match 26.3%; Score 601.8; DB 6; Length 693;
Best Local Similarity 92.4%; Pred. No. 2.3e-129;
Matches 633; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy 1589 GAGCGCGCTCGAGGAGTCTCAATCCATCCGCAACAGCTTCTCGGGTCCCTCGCT 1648
Db 8 GAGCGCGCTCGAGGAGTCTCAATCCATCCGCAACAGCTTCTCGGGTCCCTCGCT 67
Qy 1649 TTCAACCGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCCAGCTTTCAGCGCAGAT 1708
Db 68 TCCACCGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCCAGTTCACACCAAGAT 127
Qy 1709 CTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTGGGAACTTCATCTCTCTGGACAAAAG 1768
Db 128 CTCTCTCTGAGCTGGCAAAACGCTCTCTGGTTGGGAAATTTTCATCTCTCTGGACAAAAG 187
Qy 1769 AACAAATATTTCTCTGCTGCTAAAGGACAACTCTCAGCAGCATCAAAAGCAGCATCTGCC 1828
Db 188 AACAAATATTTCTCTGCTGCTAAAGGACAACTCTCAGCAGCATCAAAAGGAGCATTTGCC 247
Qy 1829 ATGCTTTTCTGCTGATCCCGAGCTCAGTCACTGCTGTGTACAGACACAGCTTCAGGG 1888
Db 248 ATGCTTTTCTGCTGATCCCGAGCTCAGTCACTGCTGTGTACAGACACAGCTTCAGGG 307
Qy 1889 CCGAGTCAAGGCGCAGTGGCGGCGCTCTCTTCCAAAAGCCGCTCCGCTTCAGGTTGG 1948
Db 308 CCGAATACAAGGCGCAGGCGGCGGCGCTCTCTTCCAAAAGCCGCTTCAGGTTGG 367
Qy 1949 ACATCAGCTCTCTGAGGTTCCAGAGCCCTCCCGGCGAGCGGCGGAGGAGTGGT 2008
Db 368 ACATCAGCTCTCTGAGGTTCCAGAGCCCTCCCGGCGAGCGGCGGAGGAGTGGT 427
Qy 2009 GCATCTACTCTCGTCACCTTCACTCTCATCTCGGCTCCCGAGCTTCAGGCGAGTGG 2068
Db 428 GCATCTACTCAGTCACCTTCACTCTCATCTCGGCTCCCGAGCTTCAGGCGAGTGG 487
Qy 2069 TGGAGACCATCCAGGCAAGCTCTCTGAGCACTCATGACAGCCCTCCGTTGAGGCCCTGG 2128
Db 488 TAGAGACCATCCAGGCAAGTGTCTGAGTACTCAGGACAGCCCTCCGTTGAGGCCCTGG 547
Qy 2129 CAGACGAGAGAGCGGGCCAGACCCGCGCTGCTGTGTGCTCCACCCCGAGCTTCGAGC 2188
Db 548 CAGATGAGAGAGAGCGGAGCCAGACCCGCGCTGCTGTGTGCTCCACCCCGAGCTTCGAGC 607
Qy 2189 CCCACCCCGCGCGCCAGACCCAGAGCTGAGCAGCTCTCTCCCGCGAGGCGGCCCCCAAGG 2248
Db 608 CCCACCCAGCGCGCTGAGACCTGATCTGATGATGCTCTCCCGCGAGGAGCCCTTAAGG 667
Qy 2249 ACAAGAGCTCTTGGCCACCAACGG 2273
Db 668 ACAAGAGCTCTTGGCCACCAATGG 692
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RESULT 9

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CO568702
LOCUS CO568702 770 bp mRNA linear EST 19-JUL-2004
DEFINITION AGENCOURT 28620318 NIH MGC 249 Rattus norvegicus cdna clone
IMAGE:7379280 5', mRNA sequence.
CO568702
ACCESSION CO568702.1 GI:50381331
VERSION
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KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 770)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: dsgerha@nih.gov
          Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
          College of Wisconsin
          cDNA Library Preparation: Open Biosystems
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM15535 row: o column: 22
          High quality sequence stop: 665.

FEATURES             Location/Qualifiers
     source           1..770
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="IMAGE:7379280"
                     /lab_host="DH10B Tona"
                     /clone_lib="NIH_MGC_249"
                     /note="Organ: spleen; Vector: pExpress-1; Site 1: EcoRV;
                     Site 2: NotI; RNA obtained from testis tissue of 8 wk old
                     animal. Tissues were snap-frozen and kept at -80C before
                     RNA extraction and purification (Tri-reagent method). cDNA
                     was primed using oligo-dT primer:
                     5'-TGACTAGTCTAGATCGGAGCGCGCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
                     resulted in an average insert size of 1.4 kb. This primary
                     library is normalized (primary library is NIH_MGC_248)
                     and was constructed by Express Genomics (Frederick, MD).
                     Note: this is a NIH_MGC library."

ORIGIN
Query Match      26.2%; Score 600; DB 7; Length 770;
Best Local Similarity 90.6%; Pred. No. 6,1e-129;
Matches 662; Conservative 0; Mismatches 66; Indels 3; Gaps 2;

QY 1469 CAGGCTCCCGCGCTCTCTGCGGGACCCCTTGCACTCGCTCTGCACACGCCCGGG 1528
Db 1 CAGGCTCCCGCGCTCTCTGCGGGACCCCTTGCACTCGCTCTGCACACGCCCTCGAG 60

QY 1529 CAGTTCACCGGGACCCCGGGGACACACACCCCGCGCGGGTGGCGTGGCGGG 1588
Db 61 CCAGCGCTACCGGGACTCCAGGAACATACACCACTCCAGCGCGCGGGTGGCGTGGCGGG 120

QY 1589 GAGCGCGCTGAGGAGTGTCTCACTCCATCCGCAACAGCTTCCTGGGCTCCCTCGCT 1648
Db 121 GAGCGCGCTGAGGAGTGTCTCACTCCATCCGCAACAGCTTCCTGGGCTCCCTCGCT 180

QY 1649 TTACCGCGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCAGCTTGACCGCAGAGT 1708
Db 181 TCCACCGCGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCAGCTTGACCGCAGAGT 240

QY 1709 CTTCCCGGAGCTGGCAAAACCTCTCTGTTGCGGAACTTCATCTCCCTTGGAACAAGAG 1768
Db 241 CCTCTCCAGAGCTGGCAAAACCTCTCTGTTGCGGAAATTCATCTCCCTTGGAACAAGAG 300

QY 1769 AACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAGAGCATCGTCC 1828
Db 301 AACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAGAGCATCGTCC 360

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QY 1829 ATGCTTTCTCTCGATCCCGAGCCTGAGTCACTGCTGCTTCAAGACAGCTTCAGGG 1888
Db 361 ATGCTTTCTCTCGATCCCGAGCCTGAGTCACTGCTGCTTCAAGACAGCTTCAGGG 420

QY 1889 CCGAGTACAAAGCCAGTGGCGCGCCCTCCGCTTCCAAAGCCCGTCCGCTTCAGGTTG 1948
Db 421 CCGAATAAAGCCAGCGGTGGCGCCCTCTGCTTCCAGAGCCCTGCTCCGCTTCAGGTTG 480

QY 1949 ACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGACGGAGCGAGTGGTG 2008
Db 481 ACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGAGATGGTAGCAGTGGAGGTG 540

QY 2009 GCATCTACTCCGTTACCTTCACTCTCATCTCGGTCCAGCGCTGGTTCAGCGAGTGG 2068
Db 541 GCATCTACTCAGTCACTTCACTCTCATCTCGGTCTAGCGCTGGTTCAGCGAGTGG 600

QY 2069 TGGAGACCATCCAGGCAGAGCTCTGAGCACTCATGACAGCCCTCCCTGCGAGGCCCTGG 2128
Db 601 TAGAGACCATCCAGGCAGAGTCTGAGTACTCATGACAGCCCTCCCTGCGAGGCCCTGG 660

QY 2129 CAGACGAGAAGAACGGGGCCAGACCCCGCTGCTGGTGGCCCGACCCCGAGAGCTGCGAC 2188
Db 661 CAGATGAGAAGA--TGGAGCCAGACCGCGCTGCTGGTACCCCA-CCGGAAGCCTGCANC 717

QY 2189 CCCACCCCGGC 2199
Db 718 TTCCCGCAGGCC 728

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RESULT 10
CV023843      615 bp mRNA linear EST 20-AUG-2004
LOCUS 878 Full Length cDNA from the Mammalian Gene Collection Homo
DEFINITION sapiens cDNA 5' similar to BC016681, mRNA sequence.
ACCESSION CV023843
VERSION CV023843.1 GI:51481642
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 615)
AUTHORS Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
          Driscoll,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
          Clingingsmith,F.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
          Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
          Vandenhaute,J., Cusick,M.E., Alcala,J.S., Hill,D.E. and Vidal,M.
          Human ORFome Version 1.1: a Platform for Reverse Proteomics
          Genome Res. (2004) In press
          Contact: Vidal M
          Marc Vidal Laboratory
          Dana Farber Cancer Institute
          1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
          Tel: 617 632 5180
          Fax: 617 632 5739
          Email: Marc.Vidal@dfci.harvard.edu
          ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
          results from a PCR reaction using an MGC full-length cDNA as
          template DNA and ORF specific primers
          PCR Primers
          FORWARD: ATGGGAGCCTGCCATCCAA
          BACKWARD: CAGGCAGAGGGTCCCGTT
          Insert length: 615 Std Error: 65.00
          Plate: 11065 row: 12 column: A
          Seq primer: ACTGCGCTGTTTACACAGTCTGTCGTCGGAAAC
          High quality sequence start: 98
          High quality sequence stop: 614
          POLYA-No.
          Location/Qualifiers
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          /organism="Homo sapiens"
          /mol_type="mRNA"

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/db_xref="taxon:9606"
/tissue_type="mixed"
/clone_lib="Full length cDNA from the Mammalian Gene
Collection"
/note="vector: mixed; The ORFs were PCR amplified from the
MGC (Mammalian Gene Collection) as of April 2004 and
cloned by recombinational Gateway cloning into pDONR223
Donor vector. Reference : MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"

ORIGIN
Query Match 26.0%; Score 595.8; DB 7; Length 615;
Best Local Similarity 99.0%; Pred. No. 5.6e-128;
Matches 609; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

Qy 868 ATGGGGAGCTTCCATCCACGGAGAGCTGACCCGACGCTCTAGAGAGCATGGCATCA 927
Db 1 ATGGGGAGCTTCCATCCACGGAGAGCTGACCCGACGCTCTAGAGAGCATGGCATCA 60

Qy 928 CTGGGCTGCTTCAGGGACCGGAGAGGCTGCATCGGAGCTGCGCAGTGTGAGGAGAGAAC 987
Db 61 CTGGGCTGCTTCAGGGACCGGAGAGGCTGCATCGGAGCTGCGCAGTGTGAGGAGAGAAC 120

Qy 988 CAAGAAAGATGATATATTATCTGCTTTTGGATCGGAAGGCGGTATCCAGCTGTGAG 1047
Db 121 CAAGAAAGATGATATATTATCTGCTTTTGGATCGGAAGGCGGTATCCAGCTGTGAG 180

Qy 1048 GACCAGGACCTGCTCCCGGAATGATGTTACACCCCGGAGAGCGTGTGATTTCTCC 1107
Db 181 GACCAGGACCTGCTCCCGGAATGATGTTACACCCCGGAGAGCGTGTGATTTCTCC 240

Qy 1108 ATGTGAGCCCTCAGGGAAGCGGACGAGAGCGGAAGTCCATGGAAGTCTCTGAGCATC 1167
Db 241 ATGTGAGTCTCAGGGAAGCGGACGAGAGCGGAAGTCCATGGAAGTCTCTGAGCATC 300

Qy 1168 ACCGATGCGGGGTGTGGTCTCCCTGTATACCAACCGAGCGGCTTGGAGATGGCCGAG 1227
Db 301 ACCGATGCGGGGTGTGGTCTCCCTGTATACCAACCGAGCGGCTTGGAGATGGCCGAG 360

Qy 1228 CACAGCAGAGATCCCGTAGGCTGAGTGAGGCTCCAGGCTCTGCTCTCCAGCCCTTA 1287
Db 361 CACAGCAGAGATCCCGTAGGCTGAGTGAGGCTCCAGGCTCTGCTCTCCAGCCCTTA 420

Qy 1288 AGCAGCCCAAGAGTCCGCTCTTTTCTTTTACCGAGCGGGGCTGAGATGAGGCT 1347
Db 421 AGCAGCCCAAGAGTCCGCTCTTTTCTTTTACCGAGCGGGGCTGAGATGAGGCT 480

Qy 1348 CGAGCGGGGCTCTCCGACTTCCAAACGAGAGCTGCTTCTTCGGGGGCCCCAGGGGT 1407
Db 481 CGAGCGGGGCTCTCCGACTTCCAAACGAGAGCTGCTTCTTCGGGGGCCCCAGGGGT 540

Qy 1408 GGGGG--CGCGGGGAGAGCGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCCGCC 1465
Db 541 GNGGGGCGCGGGGAGAGCNCGCCGCCCGCCAGTGCCTCCACACCCCTGCGCCGCC 600

Qy 1466 CCCAGGCTCCCCCGC 1480
Db 601 CCCAGGCTCCCCCGC 615

RESULT 11
BM948524
LOCUS
DEFINITION UI-M-EG0p-bve-1-10-0-UI.r1 NIH_BMAP_EG0p Mus musculus cDNA clone
IMAGE:5691033 5', mRNA sequence.
ACCESSION BM948524
VERSION BM948524.1 GI:19432115
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 698)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@pds-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyx-5.
Location/Qualifiers
1..698
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5691033"
/tissue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EG0p"
/note="Organ: brain; Vector: pyx-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is CAGCCACGAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institute of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Query Match 25.9%; Score 592.4; DB 5; Length 698;
Best Local Similarity 90.5%; Pred. No. 3.5e-127;
Matches 632; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 284 AGCAGCTCTCGGGGTGAGCTATTCGACTACCTGGTAAAGAGGGGAGACTGACGCCA 343
Db 1 AGCAGCTTCTGCTGTGTGAGCTGTTTCGACTACCTGGTAAAGAGGGGAGACTGACGCCA 60

Qy 344 AGGAGGCCGGAAGTCTTCGCCAGATTTGCTCGCTGCGTGGACTTCTGCCACAGCTACT 403
Db 61 AGGAGGCCGGAAGTCTTCGCCAGATTTGCTCGCTGCGTGGACTTCTGCCACAGCTACT 120

Qy 404 CCATCTGCACAGAGACTTAAAGCCGAGAACCTGCTTTTGGATGAGAAAAACAACATCC 463
Db 121 CCATCTGCACAGAGACTTAAAGCCGAGAACCTGCTTTTGGATGAGAAAAACAACATCC 180

Qy 464 GCATTGAGACTTTCGGCATGCGCTCCCTGCGAGTGGGGGACAGCCTCTCTGAGACCACT 523
Db 181 GCATCGCAGACTTTGGTATGGCGTCCCTGCAAGTGGGGGACAGCCTCTCTGAGACCACT 240

Qy 524 CGGGGTCCCCCATATATGCGTGTCCAGAGTGTATTAAGGGGGAATAATATATGCGCCGC 583
Db 241 CGGGGTCCCCCATATATGCGTGTCCAGAGTGTATTAAGGGGGAATAATATATGCGCCGC 300

Qy 584 GGGCAGACATGTGGAGCTGTGGAGTCACTCTCTTTCGCCCTCTGCTGGGGGCTCTGCCCT 643
Db 301 GGGCAGACATGTGGAGCTGTGGAGTCACTCTCTTTCGCCCTCTGCTGGGGGCTCTGCCCT 360
```

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
```


5'-pGATAGTCTTAGATCGAGCGCGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 1.7 kb. This primary library is a normalized (primary library is NIH MGC 254) and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"

ORIGIN	Query Match	25.3%	Score 579.8;	DB 7;	Length 693;
	Best Local Similarity	90.6%	Pred. No. 3.1e-124;		
	Matches 628;	Conservative 0;	Mismatches 64;	Indels 1;	Gaps 1;
QY	1383	GCTGCTTCTCGGGGCCCCAGGGTGGGGGCGCGGAGCAGCCCGCCCGCCAGTGC 1442			
Db	1	GCTGCTTCTCGGGGCCCCAGAGGTGGGGGCGCTGGAGAGCAGCCACCACTCCCGTGC 60			
QY	1443	CGGCTCCACACCCCTCGCGGCCCGCCAGAGTCCCGCGGCTCTCTGCGGGAGACCCCTT 1502			
Db	61	CGGTTCCAGCCCTTGGCTGGACACACAGGTCTCCCGGCTCTCCGGGGAAACCCCTT 120			
QY	1503	GCACCTGCTCTGACACAGCCCGCGGCCAGTCCCAACCGGGACCCCGGGGACAAACACC 1562			
Db	121	GCACCTCACCTCTGACACAGCCCTCGAGCCAGCCCTACCGGGAATCCAGGAACCTACCA 180			
QY	1563	CCCGAGCCCGCGGTGGGCTCGGGGAGCGCCCTGGAGAGTCTCTCAACTCCATCCG 1622			
Db	181	TCCAGCCCGAGCGGTGGGCTCGGGGAGCGCCCTGGAGAGTCTCTCAACTCCATCCG 240			
QY	1623	CAACAGTCTCTGGGCTCCCGCTCGCTTTCACCGGCGCAAGATGCAAGTCCCTACCGCTGA 1682			
Db	241	CAACAGTCTCTGGGCTCCCGCTCGCTTTCACCGGCGCAAGATGCAAGTCCCTACCGCTGA 300			
QY	1683	GGAGATGTCCAGTTGACCGCCAGAGTCTCCCGGAGCTGGCAAAACGCTCTGGTTCGG 1742			
Db	301	GGAGATGTCCAGTTGACACACCAAGATTCCTCCAGAGCTGGCAAAACGCTCTGGTTCGG 360			
QY	1743	GAATCTATCTCTCTCGACAAAGAAACAATAATTCCTCTGCTGCTAAAGGACAAACCTCT 1802			
Db	361	GAATCTATCTCTCTCGACAAAGAAACAATAATTCCTCTGCTGCTAAAGGACAAACCTCT 420			
QY	1803	CAGCAGCATCAAAAGCAGACATGCTCATGCTTTCTGTGATCCCGAGCTGAGTCAAG 1862			
Db	421	CAGCAGCATCAAAAGCAGACATGCTCATGCTTTCTGTGATCCCGAGCTGAGTCAAG 480			
QY	1863	TGTGCTGTACACACCAAGCTTTCAGGCGCCAGTAAAGGCGGCGGCGCCCTCCGCTTT 1922			
Db	481	TGTGCTGTACACACCAAGCTTTCAGGCGCCAGTAAAGGCGGCGGCGGCGCCCTCCGCTTT 539			
QY	1923	CCAAAGCCGCTCCGCTTCCAGGTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCG 1982			
Db	540	CCAGAGCCTGTCCGCTTCCAGGTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCG 599			
QY	1983	GCAGCGGAGCGGAGCGGAGGTGGTGGCATCTACTCGTCACCTTCACTCTCATCTCGGG 2042			
Db	600	CCGAAGAGATGTAGCAGTGGAAAGTGGCATCTACTCAGTCACCTTCACTCTCATCTCGG 659			
QY	2043	TCCAGCGCTCGGTTCAAGCGAGTGGTGGAGAC 2075			
Db	660	TCCTAGCCGCTCNGTCAAGCGTGTGGTAGAGAC 692			

RESULT 13
BM944329
LOCUS
DEFINITION
UI-M-EH0p-bvq-d-01-0-UI.r1 NIH_BMAP_EH0p Mus musculus cDNA clone
IMAGE:5695440 5', mRNA sequence.
ACCESSION
BM944329
VERSION
BM944329.1
GI:19427914
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

QY	644	TTGATGACGACAACTCCCGCAGCTGCTGGAGAGGTGAACCGGGCGCTCTCCCATGC 703			
Db	361	TCGATGACGACAACTCCCGCAGCTACTGGAGAAGGTGAACGTGGGTCTTCCCATGC 420			
QY	704	CCACATTCATCTCCAGATTGCAGAGCTCTCTGAGGGGAATGATCGAAGTGGAGCCCG 763			
Db	421	CTCACTTCATCTCCAGACTGCAGAGCTCTCTGAGGGGAATGATCGAAGTGGAGCCCG 480			
QY	764	AAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAATCTTGGTACCTAGGGGGGAACAG 823			
Db	481	AGAAAGGCTCAGTCTGGAGCAAAATTCAGAAAATCTTGGTATCTGGGGGGAACAG 540			
QY	824	AGCAGACCGTCTGCTGGAGCCAGCCCTCGCGCGGTAGCATGCGGAGCTGCGCAT 883			
Db	541	AACAGACCGTCTGCTGGAGCCAGCCCTCGCGCGGTAGCATGCGGAGCTGCGCAT 600			
QY	884	CCACGAGAGCTGGAACCCCGAGCTCTCTAGAGAGCATGGCATCACTGGGCTGCTCAGGG 943			
Db	601	CCATGGCGAGCTGGAACCCCTGAGCTTCTGGAAAGCATGGCGTCTCTGGGCTGCTCAGAG 660			
QY	944	ACCAGAGAGCTGCATCGGAGCTGCGGAGTGGCGAGTGAAGAG 981			
Db	661	ACCAGAGAGCTGCATCGAGAGAACTGCGAAGCGAGAG 698			

RESULT 12
CO393904
LOCUS
DEFINITION
AGENCOURT 26730340 NIH MGC 255 Rattus norvegicus cDNA clone
IMAGE:7320287 5', mRNA sequence.

ACCESSION
CO393904
VERSION
CO393904.1
KEYWORDS
EST.
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 693)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM15382 row: e column: 21
High quality sequence stop: 519.
Location/Qualifiers

FEATURES
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1..693
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7320287"
/sex="both"
/tissue_type="Brain - Pooled from several tissues from one
or more individuals"
/lab_host="DH10B rona"
/clone_lib="NIH MGC 255"
/notes="Organ: brain/CNS; Vector: pExpress-1; Site_1:
EcoRV; Site_2: NotI; RNA obtained from brain tissue of 8
wk old animal. Tissues were snap-frozen and kept at -80C
before RNA extraction and purification (Tri-reagent
method). cDNA was primed using oligo-dT primer:

REFERENCE 1 (bases 1 to 742)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
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 Seq primer: pYX-5.
 Location/Qualifiers
 1..742
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:5695440"
 /tissue_type="whole brain"
 /dev_stage="embryo 18.5 dpc"
 /lab_host="DH10B (TI phage resistant)"
 /clone_lib="NIH_BMAP_EH0p"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCAGCAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
 Query Match 25.1%; Score 574.8; DB 5; Length 742;
 Best Local Similarity 89.4%; Pred. No. 4.6e-123;
 Matches 663; Conservative 0; Mismatches 74; Indels 5; Gaps 4;

394 CACAGCTACTCCATCTGCCACAGACCTTAAGCCCGAGACCTGCTTTGGATGAGAAA 453
 2 CATAGCTACTCCATCTGTACAGAGACTTGAAGCCAGAGAACCTGCTTTGGATGAGAAA 61
 454 AACAACTCCCATTTGACAGACTTCGGCATGCGCTCCCTGCAGGTGGGGCAGACCTCTG 513
 62 AACAACTCCCATTCGAGACTTTGGTATGCGGTCCCTGCAAGTGGGGCAGACCTCTG 121
 514 GAGACCACTGCGGGTCCCCCATTTATCGTGTCCAGAGGTGATTAAGGGGAAAAATAT 573
 122 GAGACCACTGCGGGTCCCCCATTTACGATGTCCAGAGGTGATCAAGGGGAAAAATAT 181
 574 GATGGCCGCGGGCAGACATGTGAGCTGTGGAGTCACTCTTCGCGCTCTCGTGGGG 633
 182 GATGGCCGCGGGCAGACATGTGAGCTGTGGAGTCACTCTTATTTGCGCTCTCTGTGGG 241
 634 GCTCTGCGCTTTGATGACGACAACTCGCCAGCTGTGGAGAGGTGCAACGGGGCGTC 693
 242 GCATGCGCTTCGATGACGACAACTCGCCAGCTGTGGAGAGGTGCAACGGGGCGTC 301
 694 TTCCACATGCCCCCACTTCATTTCCATGTCAGAGCTCTCTCAGGGGAATGATCGAA 753
 302 TTCCACATGCTCACTTCATCTCCAGACTGCCAGAGCTCTCTGAGAGGATGATGAA 361
 754 GTGGAGGCCGAAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGTA--CCTAG 811

Db 362 GTGAGGCCGAGAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTTGGTATCNTGG 421
 Qy 812 GCGGGAACACGAGCCAGACCCGTCCTGGAGCCAGGCCCTTGGCGCGCGGTAGGCATGC 871
 Db 422 GCGGGAACACGAGCCAGACCCCTTGGCTGGAGCCAGCCCGCCAGAGTAGGCATGC 481
 Qy 872 GGAGCCTGCCATCAACGAGAGAGCTGGACCCCGACGCTCTAGAGAGCATGTCATCTGG 931
 Db 482 GTAGCCTGCCATCAACGAGAGAGCTGGACCCCGACGCTCTAGAGAGCATGTCATCTGG 541
 Qy 932 GCTCTTCAGAGCCGCGAGAGGCTGCATCGCAGCTGCGCAGTGAGGAGAGAACCAAG 991
 Db 542 GCTCTTCAGAGCCGCGAGAGGCTGCATCGCAGAGTGCACAGAACTGCGAAGCAGAGGAACCAAG 601
 Qy 992 AAAAGATGATATATTTATCTGC--TTTGGATCGGAAGGAGCGGTATCCAGCTGTGAGGAC 1050
 Db 602 AAAAGATGATCTATTTATTTTGTCTTTGGATCGGAAGGAGCGGTATCTAGCTGTGAAGAC 661
 Qy 1051 CAGGACCTGCTCCCGGAATGATGTTGACCC--CCCCGGGAAGCGTGTGGATTTCTCCCAT 1109
 Db 662 CAGGA-CTGCTCTCTCGGAATGATGTTGACCCACCTCCGAGGCGTGTGGATTTCCCCCAT 720
 Qy 1110 GCTGAGCCGCTCACGGGAAGCGG 1131
 Db 721 GCTGAGCANACACGGGAACGG 742

RESULT 14
 LOCUS CA319620 686 bp mRNA linear EST 09-JUL-2003
 DEFINITION UI-M-FW0-cca-c-12-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
 IMAGE:6816805 5', mRNA sequence.
 ACCESSION CA319620
 VERSION CA319620.1 GI:24537744
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 686)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
 source
 Seq primer: pYX-5.
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 /lab_host="DH10B (TI phage resistant)"
 /clone_lib="NIH_BMAP_FW0"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGGAGACGAC. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

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Best Local Similarity 91.3%; Pred. No. 2.9e-122;
Matches 627; Conservative 0; Mismatches 58; Indels 2; Gaps 2;

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QY 1495 ACCCCCTTGCACCTCGCTCTGCACACGCCCGCGGCCAGTCCACCGGGACCCCGGGGACA 1554
DB 60 AACCCCTTGCACCTCACCTCTGCACCGCTCGAGCCAGCCCTACGGGACCCCGAGNACG 119

QY 1555 ACACCAACCCCGACCCCGCGGCGTGGCGTGGGGAGCGCGCTGGAGAGTCTGTCTCAAC 1614
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QY 1615 TCCATCCGACACAGCTTCCCTGGCTCCCTCGCTTTCACCGCGCGCAGATGCGAGTCCCT 1674
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QY 1735 TGGTTCGGGAATTCATCTCTCTTGGACAAGAGAAACAATAATTCCTCGTCTAAAGGAC 1794
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QY 1795 AAACTCTCAGCAGCATCAAGCAGACATGCTCATGCTCTCTGTCATCCCGAGCTG 1854
DB 360 AAACCTCTCAGCAGCATCAAGCAGGACATGCTCATGCTCTCTGTCATCCCGAGCTG 419

QY 1855 AGTCACAGTGTGCTGCACAGACAGAGCTTCAGGGCCGAGTACAGGCCAGTGGCGGCC 1914
DB 420 AGTCACAGTGTGCTGCACAGACAGAGCTTCAGGGCCGAGTACAGGCCAGTGGCGGCC 479

QY 1915 TCCGCTTTCGAAAAGCCGCTCCGCTTCAGGTGACATCAGCTCTCTGAGGGTCCAGAG 1974
DB 480 TCCGCTTTCGAAAAGCCGCTTCGCTTCAGGTGACATCAGCTCTCTGAGGGTCCAGAA 539

QY 1975 CCCTC-CCCGCGAGCGGACGCGAGGTGGTGGCATCTACTCCGTCACCTTCACTCT 2033
DB 540 CCCTCAGCCGCGGAGAGATGGCAGCAGTGGAGGTGGCATCTACTCAGTCACTTCACTCT 599

QY 2034 CATCTCCGGTCCAGCCGCTCGGTTCAACGCTGTGTAGAGACCATCCAGGACAGCTCT 2093
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QY 2094 GAGCACTCATGACAGCGCTCCGTTGCA 2120
DB 660 GAGTACTCACGACAGCGCTCCGTTGCA 686
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RESULT 15
BP251302
LOCUS BP251302 Sugano cDNA library, hippocampus Homo sapiens cDNA clone
DEFINITION HPR07089, mRNA sequence.
ACCESSION BP251302
VERSION BP251302.1 GI:52133583
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 596)

Suzuki Y., Yanashita R., Shirota M., Sakakibara Y., Chiba J.,

Mizushima-Sugano J., Nakai K. and Sugano S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuk@ims.u-tokyo.ac.jp.

Location/Qualifiers

FEATURES

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1..596

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/mol_type="mRNA"

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/clone="HPR07089"

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Best Local Similarity 99.5%; Pred. No. 5.9e-122;
Matches 593; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

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QY 473 ACTTCGGCATGGCGTCCCTGCAGTGGGGAGACGCTCTCTGGAGACGAGCTGGGGTCCC 532
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QY 533 CCATATATGCTGTCCAGAGGTGATTAAAGGGGAAAAATATATGATGGCGCGGCGCAGACA 592
DB 181 CCATATATGCTGTCCAGAGGTGATTAAAGGGGAAAAATATATGATGGCGCGGCGCAGACA 240

QY 593 TGTGGAGCTGTGGAGTCATCTCTTCGCTCTGCTGGGGGCTCTGCTCTTTGATGACG 652
DB 241 TGTGGAGCTGTGGAGTCATCTCTTCGCTCTGCTGGGGGCTCTGCTCTTTGATGACG 300

QY 653 ACAACCTTCGCCAGCTGCTGGAGAGGTGAAACGGGGCGCTTCCACATGCCCCACTTCA 712
DB 301 ACAACCTTCGCCAGCTGCTGGAGAGGTGAAACGGGGCGCTTCCACATGCCCCACTTCA 360

QY 713 TTCTCCAGATTCCAGAGCTCTCAGGGGAATGATCGAAGTGGAGCCCGAAAAAGGC 772
DB 361 TTCTCCAGATTCCAGAGCTCTCAGGGGAATGATCGAAGTGGAGCCCGAAAAAGGC 420

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DB 421 TCAGTCTGGAGCAAAATTCAGAAAATCTTTGGTACCTTAGCGGGAAACACAGCCAGACC 480

QY 833 CGTGCCTGGAGACCGACCCCTGGCGCGGGTAGCCATGCGGAGCTGCCATCCACCGAG 892
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QY 893 AGCTGGACCCCGAGCGTCTTAGAGAGCATGTCATCCTGCGGCTGCTTCAGGAGACCGC 948
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: February 19, 2005, 12:29:10 , Search time 1209 Seconds
(without alignments)
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Perfect score: 2289
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Scoring table: IDENTITY_NUC
Gapex 10.0 , Gapex 1.0

Searched: 5384158 seqs, 2955248155 residues
Total number of hits satisfying chosen parameters: 10768316

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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30	551	24.1	906	17	US-10-276-774-72	Sequence 72, Appli
31	512	22.4	512	9	US-09-960-253-87	Sequence 87, Appli
32	408.4	17.8	584	16	US-10-029-386-6329	Sequence 6329, Ap
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39	202.2	8.8	3170	17	US-10-276-645-1	Sequence 1, Appli
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ALIGNMENTS

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; Sequence 3, Application US/10116326
; Publication No. US20030166889A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20030166889A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0332-05A
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2289
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-116-326-3

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Matches 2289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2281 CTGCCCTGA 2289

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; Publication No. US20040180416A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/803,277
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/10/116,326
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2289
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-277-3

Query Match 100.0%; Score 2289; DB 18; Length 2289;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 TGCCACAGGAGCCAGTGGGAATGGGAGACAGAGCCCTTTGGTCTCCACATGCCCCCTTC 240
Db 181 TGCCACAGGAGCCAGTGGGAATGGGAGACAGAGCCCTTTGGTCTCCACATGCCCCCTTC 240

Qy 241 CAGCCCTCTGCCCTCTATATCTTTAGGTACCTGTTCTGGAGCAGTCTCGGGGGT 300
Db 241 CAGCCCTCTGCCCTCTATATCTTTAGGTACCTGTTCTGGAGCAGTCTCGGGGGT 300

Qy 301 GAGCTATTTCGACTACTGTTAAAGAGGGAGACTGACGCCCAAGAGAGGCCCGGAAAGTTTC 360
Db 301 GAGCTATTTCGACTACTGTTAAAGAGGGAGACTGACGCCCAAGAGAGGCCCGGAAAGTTTC 360

Qy 361 TTCCGCGCAGATTGTTCTGCGCTGGACTTTGTCACAGCTACTCATCTGCGCAGAGAC 420
Db 361 TTCCGCGCAGATTGTTCTGCGCTGGACTTTGTCACAGCTACTCATCTGCGCAGAGAC 420

Qy 421 CTAAGCCCGAGAACCTGCTTTTGGATGAGAAACACATCCGCATTCGAGACTTCGGC 480
Db 421 CTAAGCCCGAGAACCTGCTTTTGGATGAGAAACACATCCGCATTCGAGACTTCGGC 480

Qy 481 ATGGCGTCCCTGAGGTGGGGAGACAGCTCTCTGGAGACAGTCTCGGGTCCCCCATTTAT 540
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Qy 541 GCGTGTCCAGAGGTGATTAAAGGGGAAAAATATATGATGCGCCCGGGCAGACATGTGGAGC 600
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Db 781 GAGCAAAATTCAGAAACATCTTGGTACTAGCGGGGAAACACAGAGCCAGACCCGTCCTG 840
Qy 841 GAGCCAGCCCTGGCGCGGTAGCCATGCGGAGCTGCCATCCAAACGAGAGCTGAC 900
Db 841 GAGCCAGCCCTGGCGCGGTAGCCATGCGGAGCTGCCATCCAAACGAGAGCTGAC 900
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Db 1801 CTGAGCAGCATCAAGACAGACATCGTCTCATGCTTTCTGTCGATCCCGAGCCTGAGTCAC 1860
QY 1861 AGTGTGTGTCAAGACAGCCTTCAGGCGCGAGTACAGGCGCAGTGGCGCGCCCTCGGTC 1920
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QY 2041 GGTCCAGCGCTCGGTTCAAGCAGTGTGGTGGCATCTACTCTCCGTCACTTCACTCTCATCTCG 2100
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RESULT 3
US-10-116-326-5
; Sequence 5, Application US/10116326
; Publication No. US2003016889A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US2003016889A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-116-326-5
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 208 GACTTCTGCGCAGACTTACTTCCATCTGCGCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG 267
QY 445 GATGAGAAAAACAACATCCGCATTGCGCATGCGGATGCGCTCTGAGGTGGGGAC 504
Db 268 GATGAGAAAAACAACATCCGCATTGCGCATGCGGATGCGCTCTGAGGTGGGGAC 327
QY 505 AGCTCTCTGAGACAGCTGCGGCTCCCGCATATGCGTGTCCAGAGGTGATTAAAGGG 564
Db 328 AGCTCTCTGAGACAGCTGCGGCTCCCGCATATGCGTGTCCAGAGGTGATTAAAGGG 387
QY 565 GAAAAATATGATGGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTTCGCCCTG 624
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Qy 1525 CGGGCCAGTCCACCGGGACCCCGGGGACACACCCCGCCAGCCCGCGGGTGGGTC 1584
Db 1348 CGGGCCAGTCCACCGGGACCCCGGGGACACACCCCGCCAGCCCGCGGGTGGGTC 1407
Qy 1585 GGGGAGCCGCTGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTCGGGTCCCGCT 1644
Db 1408 GGGGAGCCGCTGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTCGGGTCCCGCT 1467
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Db 1708 AGGGCCAGTACAAGGCGAGTGGGGGCGCCCTCCGCTTCCAAAGACCGCTCCGTTCCAG 1767
Qy 1945 GTGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGAGCGGAGGT 2004
Db 1768 GTGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGAGCGGAGGT 1827
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Db 1948 CTGGCAGACGAGAGAAACGGGGCCAGACCCGGCTGTGTGTGCCCCACCCCGAAGCCTG 2007
Qy 2185 CAGCCCCCAGCCGGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCCCCC 2244
Db 2008 CAGCCCCCAGCCGGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCCCCC 2067
Qy 2245 AAGGACAAAGTCTCTGGCCACCAAGCGGACCCCTCTGCCCTGA 2289
Db 2068 AAGGACAAAGTCTCTGGCCACCAAGCGGACCCCTCTGCCCTGA 2112
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RESULT 4

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US-10-803-277-5
; Sequence 5, Application US/10803277
; Publication No. US20040180416A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/803,277
; PRIOR FILING DATE: 2004-03-18
; PRIOR FILING DATE: 2002-04-04
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; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-803-277-5
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Query Match 88.3%; Score 2020.2; DB 18; Length 2112;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 265 TTATAGTACTGTCTCTGAGACAGCTCTCGGGGGTGTAGCTATTCGACTACTCTCGTAAAG 324
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QY 2245 AAGGACAAAGAGCTCTCGGCCACCAACGGGACCCCTCTGCCCCGA 2289
Db 2068 AAGGACAAAGAGCTCTCGGCCACCAACGGGACCCCTCTGCCCCGA 2112
RESULT 5
US-10-116-326-1
; Sequence 1, Application US/10116326
; Publication No. US20030166889A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fridtle, Carl Johan
; TITLE OF INVENTION: No. US20030166889A1el Human Kinases and Polynucleotides Encoding t
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2337
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-116-326-1
Query Match 88.3%; Score 2020.2; DB 16; Length 2337;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 265 TTTAGGTACTGGTTCTGGAGCACGTCCTCGGGGGTGGAGTATTCGACTACCTGGTAAAG 324
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Db 553 AGCTCTCGAGACCCAGCTCGGGTCCCGCCATTATGCGTGTCCAGAGTGAATAGGGG 612
QY 565 GAAAAATATGATGGCGCCGGGAGACATGTGAGCTGTGGAGTCACTCTTCGCCCTG 624
Db 613 GAAAAATATGATGGCGCCGGGAGACATGTGAGCTGTGGAGTCACTCTTCGCCCTG 672
QY 625 CTGTTGGGGCTCTGCCCTTTTGATGACACAACTCCGCGAGCTGTGGAAGAGGTGAAA 684
Db 673 CTGTTGGGGCTCTGCCCTTTTGATGACACAACTCCGCGAGCTGTGGAAGAGGTGAAA 732
QY 685 CGGGCGCTCTTCCACATGCCCCCACTTCCTCCAGATTGCCAGAGCTCTCGTAGGGGA 744
Db 733 CGGGCGCTCTTCCACATGCCCCCACTTCCTCCAGATTGCCAGAGCTCTCGTAGGGGA 792
QY 745 ATGATCGAAGTGGAGCCCGGAAAGGCTCAGTCTGGAGCAAAATTCAAGAACATCTCTGG 804
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Db 853 TACCTAGCGGGAAACACGAGCCAGACCCGTCCTGGAGCCAGCCCTTGGCCCGCGGTA 912
QY 865 GCCATGCGGAGCTGCGCATTCACAGGAGCTGAGACCCCGAGCTCTTAGAGAGCATGGCA 924

Db 913 GCCATGGCGAGCTGCCATCCAAACGAGAGCTGGACCCCGACGTCCTTAGAGAGCATGGCA 972
Qy 925 TCACCTGGGCTGCTTCAAGGACCGGAGAGGCTGATCGCGAGCTGCGCAGTGAAGAGAG 984
Db 973 TCACTGGGCTGCTTCAAGGACCGGAGAGGCTGATCGCGAGCTGCGCAGTGAAGAGAG 1032
Qy 985 AACCAAGAAAGATGATATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1044
Db 1033 AACCAAGAAAGATGATATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1092
Qy 1045 GAGGACCAAGGACCTGCCCTCCCGGAATGATTTGACCCCCCGGAAGCGGTGATTTCT 1104
Db 1093 GAGGACCAAGGACCTGCCCTCCCGGAATGATTTGACCCCCCGGAAGCGGTGATTTCT 1152
Qy 1105 CCAATGTGAGCGCTCAGGGAACGGGAGCACAGAGGGAAGTCCATGAAGTCTCTGAGC 1164
Db 1153 CCAATGTGAGCGCTCAGGGAACGGGAGCACAGAGGGAAGTCCATGAAGTCTCTGAGC 1212
Qy 1165 ATACCGGATGCGGGGTGGTCTCCCTCTGACCCACCGAGCGGCTTGGAGATGGCC 1224
Db 1213 ATACCGGATGCGGGGTGGTCTCCCTCTGACCCACCGAGCGGCTTGGAGATGGCC 1272
Qy 1225 CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCTCCACGGGTCTGTCTCCAGGCCCT 1284
Db 1273 CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCTCCACGGGTCTGTCTCCAGGCCCT 1332
Qy 1285 CTAAGACGCCCAAGGAGTCGGTCTTTTCTTTTTCACCGGAGCGGGGGTGGAGATGAG 1344
Db 1333 CTAAGACGCCCAAGGAGTCGGTCTTTTCTTTTTCACCGGAGCGGGGGTGGAGATGAG 1392
Qy 1345 GCTCAGGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTCCGGGGCCCGAGG 1404
Db 1393 GCTCAGGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTCCGGGGCCCGAGG 1452
Qy 1405 GGTGGGCGCGCGGGAGCAGCCCCCGCCCCAGTGCCTCCACACCCCTGCCCGGC 1464
Db 1453 GGTGGGCGCGCGGGAGCAGCCCCCGCCCCAGTGCCTCCACACCCCTGCCCGGC 1512
Qy 1465 CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTGCACTCGCTCTGCAACACGCC 1524
Db 1513 CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTGCACTCGCTCTGCAACACGCC 1572
Qy 1525 CGGGCAGTCCACCGGGACCCCGGGACACACACCCCGCCAGCGCGGGGGTGGGTC 1584
Db 1573 CGGGCAGTCCACCGGGACCCCGGGACACACACCCCGCCAGCGCGGGGGTGGGTC 1632
Qy 1585 GGGGAGCGGCTGGAGAGTCTCACTCACTCCATCGCAACAGCTTCTGGGCTCCCT 1644
Db 1633 GGGGAGCGGCTGGAGAGTCTCACTCACTCCATCGCAACAGCTTCTGGGCTCCCT 1692
Qy 1645 CGCTTTACCGGCGCAAGATGAGTCCCTACCGCTGAGGAGTGTCCAGTTGACGCCA 1704
Db 1693 CGCTTTACCGGCGCAAGATGAGTCCCTACCGCTGAGGAGTGTCCAGTTGACGCCA 1752
Qy 1705 GAGTCTCTCCCGGAGCTGGCAAAAGCTCTGGTTCCGGAACTTCATCTCTTGGACAAA 1764
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Qy 1765 GAAGAACAAATATTTCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGCATC 1824
Db 1813 GAAGAACAAATATTTCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGCATC 1872
Qy 1825 GTCCATGCTTTCTGTGATCCCCAGGCTGAGTCAAGTGTGTGTGTCACAGACAGCTTC 1884
Db 1873 GTCCATGCTTTCTGTGATCCCCAGGCTGAGTCAAGTGTGTGTGTCACAGACAGCTTC 1932
Qy 1885 AGGCGCAGTACAAAGCCAGTGGGCGCCCTCCGTCTTCCAAAAGCCGCTCCGTTCCAG 1944
Db 1933 AGGCGCAGTACAAAGCCAGTGGGCGCCCTCCGTCTTCCAAAAGCCGCTCCGTTCCAG 1992
Qy 1945 GTGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGCGACGGAGCGGAGGAGGT 2004
Db 1993 GTGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGCGACGGAGCGGAGGAGGT 2052

RESULT 6

US-10-423-543-12

; Sequence 12, Application US/10423543

; Publication No. US20040058355A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc.

; APPLICANT: Libermann, Rosana K.

; APPLICANT: Hunter, John J.

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Rudolph-Owen, Laura A.

; APPLICANT: Curtiss, Rory A.J.

; APPLICANT: Olandt, Peter J.

; APPLICANT: Tsai, Fong-Ying

; APPLICANT: Galvin, Katherine M.

; APPLICANT: Chun, Miyoung

; APPLICANT: Williamson, Mark J.

; APPLICANT: Silos-Santiago, Immaculada

; APPLICANT: Bandaru, Rajasekhara

; TITLE OF INVENTION: NOVEL 1910, 56634, 55053, 2504, 15977,

; TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638.

; TITLE OF INVENTION: 18610, 33217, 21967, h1983, m1983, 38555 OR 593 MOLECULES

; TITLE OF INVENTION: AND USES THEREFOR

; FILE REFERENCE: MP103-023OMNIM

; CURRENT APPLICATION NUMBER: US/10/423,543

; CURRENT FILING DATE: 2003-04-25

; PRIOR APPLICATION NUMBER: US 10/278,036

; PRIOR FILING DATE: 2002-10-22

; PRIOR APPLICATION NUMBER: US 09/711,216

; PRIOR FILING DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: US 60/205,447

; PRIOR FILING DATE: 2000-05-19

; PRIOR APPLICATION NUMBER: US 10/012,055

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/248,325

; PRIOR FILING DATE: 2000-11-14

; PRIOR APPLICATION NUMBER: US 10/003,690

; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/248,893

; PRIOR FILING DATE: 2000-11-15

; PRIOR APPLICATION NUMBER: US 09/797,039

; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: US 60/186,061

; PRIOR FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: US 10/217,168

; PRIOR FILING DATE: 2002-08-12

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 119

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 2337

; TYPE: DNA

; ORGANISM: Homo Sapiens									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (1)...(2337)									
US-10-423-543-12									
Query Match									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
Length 2337;									
Qy	265	TTTAGGTACCTGGTTCTGGAGCACGTCCTGGGGGGGTGAGCTATTGCACTACCTGGTAAAG	324						
Db	313	TAITTTGTAATCTGGTTCTGGAGCACGTCCTGGGGGGGTGAGCTATTGCACTACCTGGTAAAG	372						
Qy	325	AAGGGGAGATGACGCGCCAAAGGAGGCCGAAAGTTCTTCGGCCAGATTGTTCTGCGCTG	384						
Db	373	AAGGGGAGATGACGCGCCAAAGGAGGCCGAAAGTTCTTCGGCCAGATTGTTCTGCGCTG	432						
Qy	385	GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG	444						
Db	433	GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG	492						
Qy	445	GATGAGAAAAAACAATCCGATTCGAGACTTCGGCATGCGCTCCCTGCGAGGTGGGGAC	504						
Db	493	GATGAGAAAAAACAATCCGATTCGAGACTTCGGCATGCGCTCCCTGCGAGGTGGGGAC	552						
Qy	505	AGCTTCTGGAGACGAGCTGGGGTCCCGCCATTATGCGTGTCCAGAGGTGATTAAAGGG	564						
Db	553	AGCTTCTGGAGACGAGCTGGGGTCCCGCCATTATGCGTGTCCAGAGGTGATTAAAGGG	612						
Qy	565	GAAAAATATGATGGCGCGGGGAGACATGTGGAGCTGTGGAGTCACTCTTTCGCCCTG	624						
Db	613	GAAAAATATGATGGCGCGGGGAGACATGTGGAGCTGTGGAGTCACTCTTTCGCCCTG	672						
Qy	625	CTCGTGGGGCTTGCCTTTTATGACGACAACTCCGCGAGCTGTGGAGTCACTCTTTCGCCCTG	684						
Db	673	CTCGTGGGGCTTGCCTTTTATGACGACAACTCCGCGAGCTGTGGAGTCACTCTTTCGCCCTG	732						
Qy	685	CGGGGGCTTTCACATGCCCTTCACTTCTCCAGATTGCCAGAGCTCTTCAGGGGA	744						
Db	733	CGGGGGCTTTCACATGCCCTTCACTTCTCCAGATTGCCAGAGCTCTTCAGGGGA	792						
Qy	745	ATGATCGAAGTGGAGCCGCAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG	804						
Db	793	ATGATCGAAGTGGAGCCGCAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG	852						
Qy	805	ATCCTAGGGGGAAACACAGAGCAGACCGCTGCTGGAGCCAGCCCTGGCGCGCGGTA	864						
Db	853	TACCTAGGGGGAAACACAGAGCAGACCGCTGCTGGAGCCAGCCCTGGCGCGCGGTA	912						
Qy	865	GCCATGCGGAGCTGCGATCCAAAGGAGAGTGGACCCCGAGCTCTTAGAGAGCATGGCA	924						
Db	913	GCCATGCGGAGCTGCGATCCAAAGGAGAGTGGACCCCGAGCTCTTAGAGAGCATGGCA	972						
Qy	925	TCACTGGGCTGCTTACGAGACCGCGAGAGGTCGATTCGGAGCTCGCAGTGGAGAGAG	984						
Db	973	TCACTGGGCTGCTTACGAGACCGCGAGAGGTCGATTCGGAGCTCGCAGTGGAGAGAG	1032						
Qy	985	AACCAAGAAAGATGATATTTATCTGCTTTTGGATCGGAAGAGCGGTATCCCACTGT	1044						
Db	1033	AACCAAGAAAGATGATATTTATCTGCTTTTGGATCGGAAGAGCGGTATCCCACTGT	1092						
Qy	1045	GAGGACACAGACCTGCTCCCGGAAATGATGTTGACCCCGGAGAGCGTGTGATTTCT	1104						
Db	1093	GAGGACACAGACCTGCTCCCGGAAATGATGTTGACCCCGGAGAGCGTGTGATTTCT	1152						
Qy	1105	CCCATGCTGAGCGTACCGGAGAGCGGACCGAGGAGTCCATGGAAGTCTCTGAGC	1164						
Db	1153	CCCATGCTGAGCGTACCGGAGAGCGGACCGAGGAGTCCATGGAAGTCTCTGAGC	1212						
Qy	1165	ATCACCGATCCGGGGGTGGTGGCTCCCTGTGTACCCACCGAGCGGCTTTGGAGATGGCC	1224						
Db	1213	ATCACCGATCCGGGGGTGGTGGCTCCCTGTGTACCCACCGAGCGGCTTTGGAGATGGCC	1272						

Qy	1225	CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCCTTCCAGGGTCTGTCTCTCAGGCCCT	1284						
Db	1273	CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCCTTCCAGGGTCTGTCTCTCAGGCCCT	1332						
Qy	1285	CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTTCACGGAGCGGGGCTGGAGATGAG	1344						
Db	1333	CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTTCACGGAGCGGGGCTGGAGATGAG	1392						
Qy	1345	GCTGAGCGGGGGCTCCCGACTTCCAAACGAGAGCTGCTTCTTCGGGGGCCAGG	1404						
Db	1393	GCTGAGCGGGGGCTCCCGACTTCCAAACGAGAGCTGCTTCTTCGGGGGCCAGG	1452						
Qy	1405	GGTGGGGGCGCGGGGAGACGCCCGCCCGCCAGTGGCCCGCTCCACACCCCTGCGCGG	1464						
Db	1453	GGTGGGGGCGCGGGGAGACGCCCGCCCGCCAGTGGCCCGCTCCACACCCCTGCGCGG	1512						
Qy	1465	CCCCCAGGCTCCCGCGCTCTCTGGGGGAGCCCTTGGCACTGGCTTCTGCAACAGGCC	1524						
Db	1513	CCCCCAGGCTCCCGCGCTCTCTGGGGGAGCCCTTGGCACTGGCTTCTGCAACAGGCC	1572						
Qy	1525	CGGGCAGTCCACACCGGAGCCCGGGGACAAACACACCCCGAGCCCGCGGGTGGGTC	1584						
Db	1573	CGGGCAGTCCACACCGGAGCCCGGGGACAAACACACCCCGAGCCCGCGGGTGGGTC	1632						
Qy	1585	GGGGGAGCGCTGGAGAGTGTCTCACTTCCATCCGCTGAGGAGATGTCCAGCTTACGCCA	1644						
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Qy	1645	CGCTTTCACCGCGCAAGATGAGTCCCTTCCGCTGAGGAGATGTCCAGCTTACGCCA	1704						
Db	1693	CGCTTTCACCGCGCAAGATGAGTCCCTTCCGCTGAGGAGATGTCCAGCTTACGCCA	1752						
Qy	1705	GAGTCTCTCCCGGAGTGGCAAAACGCTCTCGTTCGGGAACTTCACTCTTGGACAAA	1764						
Db	1753	GAGTCTCTCCCGGAGTGGCAAAACGCTCTCGTTCGGGAACTTCACTCTTGGACAAA	1812						
Qy	1765	GAAGAACAAATATTCCTCGTCTAAAGGACAAACCTCTCAGCAGATCAAAAGCAGATC	1824						
Db	1813	GAAGAACAAATATTCCTCGTCTAAAGGACAAACCTCTCAGCAGATCAAAAGCAGATC	1872						
Qy	1825	GTCCATGCTCTTCTGTGATCCCGCAGCTGAGTCAAGTGTGTGTCAAGACAGCTTTC	1884						
Db	1873	GTCCATGCTCTTCTGTGATCCCGCAGCTGAGTCAAGTGTGTGTCAAGACAGCTTTC	1932						
Qy	1885	AGGGCCGAGTCAAGGCGAGTGGCGCGCTCGCTTCCAAAGCCGCTCGCTTCCAG	1944						
Db	1933	AGGGCCGAGTCAAGGCGAGTGGCGCGCTCGCTTCCAAAGCCGCTCGCTTCCAG	1992						
Qy	1945	GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGACCGGAGGAGT	2004						
Db	1993	GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGACCGGAGGAGT	2052						
Qy	2005	GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCCGAGCGCTCGGTTCAAGCGA	2064						
Db	2053	GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCCGAGCGCTCGGTTCAAGCGA	2112						
Qy	2065	GTGCTGAGACCATCCAGGACAGCTCTGAGCACTCATGACAGCGCTCCGTTGACGGCC	2124						
Db	2113	GTGCTGAGACCATCCAGGACAGCTCTGAGCACTCATGACAGCGCTCCGTTGACGGCC	2172						
Qy	2125	CTGGCAGACGAGAGAAACGGGGGCCAGACCCGGCTGTGCTGGTCCCGACCCGAGCGCTG	2184						
Db	2173	CTGGCAGACGAGAGAAACGGGGGCCAGACCCGGCTGTGCTGGTCCCGACCCGAGCGCTG	2232						
Qy	2185	CAGCCCCACCCGGCGCCAGACCCAGAGTGGAGCTCTCCCGCGAGGCGCCCGCC	2244						
Db	2233	CAGCCCCACCCGGCGCCAGACCCAGAGTGGAGCTCTCCCGCGAGGCGCCCGCC	2292						
Qy	2245	AAGGACAAAGAGTCTCTGGGCCACCAACGGGACCCCTCTGCGCTGA	2289						
Db	2293	AAGGACAAAGAGTCTCTGGGCCACCAACGGGACCCCTCTGCGCTGA	2337						


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Db 2053 GGTGGCATCTACTCGCTCACTTCACTCTCATCTCGGGTCCAGCGCTCGGTTCAAGCGA 2112
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Db 2113 GTGGTGAGACATCCAGGCACAGCTCCCTGAGCACTCATGACAGCCCTCCGTCGAGGCC 2172
Qy 2125 CTGSCACAGCAGAGAACGAGGCGCCAGACCCCGCCTGCTGGTGCCCAACCCGAGGCTG 2184
Db 2173 CTGSCACAGCAGAGAACGAGGCGCCAGACCCCGCCTGCTGGTGCCCAACCCGAGGCTG 2232
Qy 2185 CAGCCCCACCCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGAGGSCCCCCC 2244
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RESULT 8
US-10-311-034-43
; Sequence 43, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAFALIA, April
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: LO, Terence P.
; APPLICANT: KHAH, Farrah A.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GREYER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeev
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
; 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0-
; 25
; NUMBER OF SEQ. ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 43
; LENGTH: 2897
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 7477486CB1
US-10-311-034-43

Query Match 88.3%; Score 2020.2; DB 17; Length 2897;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 325 AAGGGAGACTGAGCCCAAGGAGGCGGAAAGTTCTTCGGCCAGAGTTGTGTCTGCCCTG 384
Db 421 AAGGGAGACTGAGCCCAAGGAGGCGGAAAGTTCTTCGGCCAGAGTTGTGTCTGCCCTG 480
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Db 481 GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAGCTCTTTTG 540
Qy 445 GATGAGAAAAACAACATCGCATTCGAGACTTCGCGCATGGCGTCCCTCGAGGTGGGAC 504
Db 541 GATGAGAAAAACAACATCGCATTCGAGACTTCGCGCATGGCGTCCCTCGAGGTGGGAC 600
Qy 505 AGCCTCTCTGGAGACAGCTGCGGGTCCCCCATATTATGCGTGTCCAGAGTGAATTAAGGG 564
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Qy 565 GAAAAATATGATGGCGCGGCGGACAGATGTGGAGCTGTGGAGTCACTCTCTTCCGCTG 624
Db 661 GAAAAATATGATGGCGCGGCGGACAGATGTGGAGCTGTGGAGTCACTCTCTTCCGCTG 720
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Qy 685 CGGGGCGTCTTCCACATGCCCCCATTTCTCCAGATTGGCCAGAGCTCTCTGAGGGGA 744
Db 781 CGGGGCGTCTTCCACATGCCCCCATTTCTCCAGATTGGCCAGAGCTCTCTGAGGGGA 840
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Db 841 ATGATCGAAGTGGAGCGCCGAAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAAATCCTTGG 900
Qy 805 TACTAGGCGGGAAACACAGAGCCAGACCCGCTGGAGCGAGCCCTCGCCCGCGGTA 864
Db 901 TACTAGGCGGGAAACACAGAGCCAGACCCGCTGGAGCGAGCCCTCGCCCGCGGTA 960
Qy 865 GCCATGCGAGCCTGCCATCCAAACGAGAGCTGGACCCGAGCTCTCTAGAGAGCATGGCA 924
Db 961 GCCATGCGAGCCTGCCATCCAAACGAGAGCTGGACCCGAGCTCTCTAGAGAGCATGGCA 1020
Qy 925 TCCTGCGGCTGCTTCAGGACCCGCGAGAGGCTGCATCGGAGCTGCGCAGTGAAGGAG 984
Db 1021 TCCTGCGGCTGCTTCAGGACCCGCGAGAGGCTGCATCGGAGCTGCGCAGTGAAGGAG 1080
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Db 1081 AACCAAGAAAAGATGATATATTATCTCTTTTGGATCGGAGGAGCGGTATCCAGCTGT 1140
Qy 1045 GAGCAGCAGGACCTGCGCTCCCGGAATGATGTTGACCCCCCCCCCGGAAGCGTGTGATCT 1104
Db 1141 GAGCAGCAGGACCTGCGCTCCCGGAATGATGTTGACCCCCCCCCCGGAAGCGTGTGATCT 1200
Qy 1105 CCCATGCTGAGCCTGACAGGAAACGCGGACCGAGCGGAGTCCATGGAAGTCTCAGC 1164
Db 1201 CCCATGCTGAGCCTGACAGGAAACGCGGACCGAGCGGAGTCCATGGAAGTCTCAGC 1260
Qy 1165 ATCACCAGTGGCGGGGTGGTGGCTCCCTGTATCCCAACCCGAGCGGCTTGGAGATGGCC 1224
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Db	1658	CGGCCAGTCCACCGGGACCCCGGGGACAAACACACCCCGGCGGCGTGCCTC	1717
QY	1585	GGGGAGCCCGCTGGAGAGTCTCTCACTCGGCAACAGCTTCTCTGGGCTCCCT	1644
Db	1718	GGGGAGCCCGCTGGAGAGTCTCTCACTCGGCAACAGCTTCTCTGGGCTCCCT	1777
QY	1645	CGCTTTCACCGGGCAGATGCGAGTCCCTACCGCTGAGGAGATGTCAGCTTGA	1704
Db	1778	CGCTTTCACCGGGCAGATGCGAGTCCCTACCGCTGAGGAGATGTCAGCTTGA	1837
QY	1705	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTGGTTCGGGAATCTCTCTGGGCA	1764
Db	1838	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTGGTTCGGGAATCTCTCTGGGCA	1897
QY	1765	GAGAACAAATATTTCTCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAA	1824
Db	1898	GAGAACAAATATTTCTCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAA	1957
QY	1825	GTCCATGCTTTCTCTGCTGATCCCGAGCTGAGTCAAGTGTGTGTCAAGAC	1884
Db	1958	GTCCATGCTTTCTCTGCTGATCCCGAGCTGAGTCAAGTGTGTGTCAAGAC	2017
QY	1885	AGGGCCGAGTACAGGCGCAGTGGCGGCCCTTCCGCTTCCAAAGCCGCTCC	1944
Db	2018	AGGGCCGAGTACAGGCGCAGTGGCGGCCCTTCCGCTTCCAAAGCCGCTCC	2077
QY	1945	GTGGACATCAGCTCTCTGAGGCTCCAGAGCCCTCCCGCGACGGGAGGCT	2004
Db	2078	GTGGACATCAGCTCTCTGAGGCTCCAGAGCCCTCCCGCGACGGGAGGCT	2137
QY	2005	GGTGGCATCTACTCCGCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCT	2064
Db	2138	GGTGGCATCTACTCCGCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCT	2197
QY	2065	GTGGTGGAGACCATCCAGGACAGCTCTCTGAGCATCATGACACCGCTCT	2124
Db	2198	GTGGTGGAGACCATCCAGGACAGCTCTCTGAGCATCATGACACCGCTCT	2257
QY	2125	CTGGCAGACGAGAGAAACGGGGCCCGAGACCGGCTGTGTGCTGCTGCTG	2184
Db	2258	CTGGCAGACGAGAGAAACGGGGCCCGAGACCGGCTGTGTGCTGCTGCTG	2317
QY	2185	CAGCCCCCAGCGGCGCCCGAGACCGGAGCTGAGCAGCTCTCCCGCGG	2244
Db	2318	CAGCCCCCAGCGGCGCCCGAGACCGGAGCTGAGCAGCTCTCCCGCGG	2377
QY	2245	AAGGACAAAGAGCTCTCTGCGCCACCAACGGGAGCCCTCTGCTGCTGA	2289
Db	2378	AAGGACAAAGAGCTCTCTGCGCCACCAACGGGAGCCCTCTGCTGCTGA	2422

RESULT 10
US-10-423-543-10
; Sequence 10, Application US/10423543
; Publication No. US20040058355A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Libermann, Rosana K.
; APPLICANT: Hunter, John J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Chun, Miyoung
; APPLICANT: Williams, Mark J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
; TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638,

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1  TITLE OF INVENTION: 18610, 33217, 21967, h1983, m1983, 38555 OR 593 MOLECULES
2  TITLE OF INVENTION:  AND USES THEREFOR
3  FILE REFERENCE: MPI03-023OMNIM
4  CURRENT APPLICATION NUMBER: US/10/423,543
5  CURRENT FILING DATE: 2003-04-25
6  PRIOR APPLICATION NUMBER: US 10/278,036
7  PRIOR FILING DATE: 2002-10-22
8  PRIOR APPLICATION NUMBER: US 09/711,216
9  PRIOR FILING DATE: 2000-11-09
10 PRIOR APPLICATION NUMBER: US 60/205,447
11 PRIOR FILING DATE: 2000-05-19
12 PRIOR APPLICATION NUMBER: US 10/012,055
13 PRIOR FILING DATE: 2001-11-13
14 PRIOR APPLICATION NUMBER: US 60/248,325
15 PRIOR FILING DATE: 2000-11-14
16 PRIOR APPLICATION NUMBER: US 10/003,690
17 PRIOR FILING DATE: 2001-11-15
18 PRIOR APPLICATION NUMBER: US 60/248,893
19 PRIOR FILING DATE: 2000-11-15
20 PRIOR APPLICATION NUMBER: US 09/797,039
21 PRIOR FILING DATE: 2001-02-28
22 PRIOR APPLICATION NUMBER: US 60/186,061
23 PRIOR FILING DATE: 2000-02-29
24 PRIOR APPLICATION NUMBER: US 10/217,168
25 PRIOR FILING DATE: 2002-08-12
26 Remaining Prior Application data removed - See File Wrapper or PALM.
27 NUMBER OF SEQ ID NOS: 119
28 SOFTWARE: FastSEQ for Windows Version 4.0
29 SEQ ID NO 10
30 LENGTH: 2980
31 TYPE: DNA
32 ORGANISM: Homo Sapiens
33 FEATURE:
34 NAME/KEY: CDS
35 LOCATION: (86) ... (2419)
36 US-10-423-543-10

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Query Match	88.3%	Score 2020.2;	DB 17;	Length 2980;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 2022;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	265	TTTATGGTACCTGGTCTCTGGACACGCTCTCGGGGGTGAGCTATTTCGACTACTCGTAAAG	324	
Db	398	TATTTTGATACCTGGTCTCTGGACACGCTCTCGGGGGTGAGCTATTTCGACTACTCGTAAAG	457	
Qy	325	AAGGGGAGACTGACGCCCAAGAGGCCCGCAAAAGTTCTTCCGCCAGATTGTCTCTGCGCTG	384	
Db	458	AAGGGGAGACTGACGCCCAAGAGGCCCGCAAAAGTTCTTCCGCCAGATTGTCTCTGCGCTG	517	
Qy	385	GACTTCTGCCACAGCTACTCCATCTGCCACAGACCTTAAAGCCCGAGAACCTCTCTTTTG	444	
Db	518	GACTTCTGCCACAGCTACTCCATCTGCCACAGACCTTAAAGCCCGAGAACCTCTCTTTTG	577	
Qy	445	GATGAGAAAAACAACATCCGCAITTCGACACTTCGGCATGGCGTCCCTGCAGGTGGGGAC	504	
Db	578	GATGAGAAAAACAACATCCGCAITTCGACACTTCGGCATGGCGTCCCTGCAGGTGGGGAC	637	
Qy	505	AGCCTCTCTGGAGACACAGCTCGGGTCCCGCCATTATGCTGCTCCAGAGGTATTAAAGGG	564	
Db	638	AGCCTCTCTGGAGACACAGCTCGGGTCCCGCCATTATGCTGCTCCAGAGGTATTAAAGGG	697	
Qy	565	GAAAAATATGATGGCCGCCGGGACAGATGTGGAGCTGTGAGTCACTCTCTTGCCCTG	624	
Db	698	GAAAAATATGATGGCCGCCGGGACAGATGTGGAGCTGTGAGTCACTCTCTTGCCCTG	757	
Qy	625	CTCGTGGGGGCTCTGCCCTTTGATGACGACAACTCCGCCAGCTGCTGGAGAAAGGTGAAA	684	
Db	758	CTCGTGGGGGCTCTGCCCTTTGATGACGACAACTCCGCCAGCTGCTGGAGAAAGGTGAAA	817	
Qy	685	CGGGGCGTCTTCACATGCCCCCACTTCACTTCTCCAGATTGCCAGAGCCTCTGAGGGGA	744	
Db	818	CGGGGCGTCTTCACATGCCCCCACTTCACTTCTCCAGATTGCCAGAGCCTCTGAGGGGA	877	

Qy	745	ATGATCGAAGTGTGAGCCCGAAAAAGGCTCAGTCTGTGAGCAAAATTGAAAGACATCTCTTGG	804
Db	878	ATGATCGAAGTGTGAGCCCGAAAAAGGCTCAGTCTGTGAGCAAAATTGAAAGACATCTCTTGG	937
Qy	805	TACCTAGCGGGGAAAACACGAGCCAGACCCCTGCTGTGAGCAGCCCTGTCGCCCGGGTA	864
Db	938	TACCTAGCGGGGAAAACACGAGCCAGACCCCTGCTGTGAGCAGCCCTGTCGCCCGGGTA	997
Qy	865	GCCATGCGGAGCCTGCCATCAACGGAGAGCTGGACCCCGACGTCCTTAGAGAGCATGGCA	924
Db	998	GCCATGCGGAGCCTGCCATCAACGGAGAGCTGGACCCCGACGTCCTTAGAGAGCATGGCA	1057
Qy	925	TCACTGGGCTGCTTCAGGGACCGCGAGAGCTGGATCGCGAGCTGCGCAGTAGGAGGAG	984
Db	1058	TCACTGGGCTGCTTCAGGGACCGCGAGAGCTGGATCGCGAGCTGCGCAGTAGGAGGAG	1117
Qy	985	AACCAAGAAAGATGATATATTATCTGCTTTTCGATCGGAAGAGCGGTATCCACGCTGT	1044
Db	1118	AACCAAGAAAGATGATATATTATCTGCTTTTCGATCGGAAGAGCGGTATCCACGCTGT	1177
Qy	1045	GAGGACCAGGACCTGCCCTCCCGGAATGATGTTGACCCCCCGGAAGCGGTATGGGATTCT	1104
Db	1178	GAGGACCAGGACCTGCCCTCCCGGAATGATGTTGACCCCCCGGAAGCGGTATGGGATTCT	1237
Qy	1105	CCCATGTGAGCCGTACAGGGAAGCGGCGACAGAGCGGAAGTCCATGGAAGTCTCTGAGC	1164
Db	1238	CCCATGTGAGCCGTACAGGGAAGCGGCGACAGAGCGGAAGTCCATGGAAGTCTCTGAGC	1297
Qy	1165	ATCACCGATCCCGGGGTGTGTGCTCCCTGTACCCACCGAGCGGGCTTTGGAGATGGCC	1224
Db	1298	ATCACCGATCCCGGGGTGTGTGCTCCCTGTACCCACCGAGCGGGCTTTGGAGATGGCC	1357
Qy	1225	CAGCACAGCCAGAGATCCCCTAGCGTCAGTGGAGCCTTCCACGGGTCTGTCTCCAGCCCT	1284
Db	1358	CAGCACAGCCAGAGATCCCCTAGCGTCAGTGGAGCCTTCCACGGGTCTGTCTCCAGCCCT	1417
Qy	1285	CTAAGCAGCCAAAGGAGTCCGGTCTTTTCTTTTACCGAGCGGGGCTGGAGATGAG	1344
Db	1418	CTAAGCAGCCAAAGGAGTCCGGTCTTTTCTTTTACCGAGCGGGGCTGGAGATGAG	1477
Qy	1345	GCTCGAGCGGGGGCTCCCGACTTCCAAAACGAGAGCTGCTTCTCGGGGCCCCAGG	1404
Db	1478	GCTCGAGCGGGGGCTCCCGACTTCCAAAACGAGAGCTGCTTCTCGGGGCCCCAGG	1537
Qy	1405	GGTGGGGGCGCGGGAGCAGCCCGCCCGCCAGTGCCTCCCAACGCTGCGCGCCG	1464
Db	1538	GGTGGGGGCGCGGGAGCAGCCCGCCCGCCAGTGCCTCCCAACGCTGCGCGCCG	1597
Qy	1465	CCCCCAGGCTCCCGCGCTCTCTGTGGGGAAGCCCTTGTGACCTCTGCAACGCGCC	1524
Db	1598	CCCCCAGGCTCCCGCGCTCTCTGTGGGGAAGCCCTTGTGACCTCTGCAACGCGCC	1657
Qy	1525	CGGGCAGTCCACCGGACCCCGGGGACAAACCAACCCCGAGCCCGCGGGTGGGTC	1584
Db	1658	CGGGCAGTCCACCGGACCCCGGGGACAAACCAACCCCGAGCCCGCGGGTGGGTC	1717
Qy	1585	GGGGGAGCCGCTTGGAGAGTCTCTCAACTCCATCGCAACAGTCTTCTGGGCTCCCTT	1644
Db	1718	GGGGGAGCCGCTTGGAGAGTCTCTCAACTCCATCGCAACAGTCTTCTGGGCTCCCTT	1777
Qy	1645	CGCTTTTCCCGGCGCAAGATGCAAGTCCCTTACCGCTGAGGAGATGTCAGCTTGAAGCCA	1704
Db	1778	CGCTTTTCCCGGCGCAAGATGCAAGTCCCTTACCGCTGAGGAGATGTCAGCTTGAAGCCA	1837
Qy	1705	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCGTTGGGAACTTTCATCTCTCTTGGACAAA	1764
Db	1838	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCGTTGGGAACTTTCATCTCTCTTGGACAAA	1897
Qy	1765	GAGGAACAAATATTCTCTGTGTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC	1824
Db	1898	GAGGAACAAATATTCTCTGTGTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC	1957
Qy	1825	GTCCATGCCTTTCTGTGATCCCGAGCCTGAGTCACAGTGTGCTGTGACAGACCGAGTTC	1884

1238 CCCATGCTGAGCGTCAACGGGAGCGGCGACCGAGCGGAGTCCATCGAAGTCTCTGAGC 1297
1165 ATACCCGATGCGGGGGTGTGGCTCCCTCTGTATCCACCCGACGCGGCTTGGAGATGGCC 1224
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1285 CTAAGCAGCCCAAGAGTCCGCTCTTTTCTTTTCAACGAGCGCGGGGCTTGGAGATGAG 1344
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1478 GCTCAGCGGGGGCTCCCGACTTCCAAACGAGAGCGTCTTCTCGGGGGCCCGAGG 1537
1405 GGTGGGGGGCGGGGAGCAGCCCGCCCGCCCGAGTCCCGCTCCACACCCCTGCCCGGC 1464
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1765 GAGAACAAATATTCCTGCTTAAGGAGCAAACTCTCAGCAGCATCAAGCAGATC 1824
1898 GAGAACAAATATTCCTGCTTAAGGAGCAAACTCTCAGCAGCATCAAGCAGATC 1957
1825 GTCCATGCTTCTGTCTGATCCCGAGCTGAGTCACTGAGTGTGTGTCACAGACAGCTTC 1884
1958 GTCCATGCTTCTGTCTGATCCCGAGCTGAGTCACTGAGTGTGTGTCACAGACAGCTTC 2017
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2018 AGGCCGAGTACAAAGGCGAGTGGCGGCCCTCTCTTCCAAAAGCCGCTCCGCTTCCAG 2077
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2078 GTGACATCAGCTCTCTGAGGTTCCAGAGCCCTCCCGGACGCGGAGCGGAGGT 2137
2005 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGTTCCAGCCGCTCGGTTCAAGCGA 2064
2138 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGTTCCAGCCGCTCGGTTCAAGCGA 2197
2065 GTGTGGAGACCATCCAGGCAAGCTCTGAGCACTCATGACAGCCCTCCGTCAGGCC 2124
2198 GTGTGGAGACCATCCAGGCAAGCTCTGAGCACTCATGACAGCCCTCCGTCAGGCC 2257
2125 CTGCGACGAGAGAAAGGGGGCCAGACCCGGGCTGTGTGTCGCCACCCCGAGGCTG 2184
2258 CTGCGACGAGAGAAAGGGGGCCAGACCCGGGCTGTGTGTCGCCACCCCGAGGCTG 2317
2185 CAGCCCCACCGGCGCCGACAGCCAGAGCTGAGAGCTCTCCCGCGGAGGCCCCCC 2244
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Qy 2245 AAGCACAAGAGCTCTGGCCACCAACGGGAGCCCTCTGCCCCTGA 2289
Db 2378 AAGCACAAGAGCTCTGGCCACCAACGGGAGCCCTCTGCCCCTGA 2422

RESULT 12

US-10-479-532-2

; Sequence 2, Application US/10479532

; Publication No. US20040151713A1

; GENERAL INFORMATION:

; APPLICANT: TAIHO PHARMACEUTICAL CO., LTD

; TITLE OF INVENTION: CELL CYCLE REGULATORY FACTOR

; FILE REFERENCE: 44B00JP

; CURRENT APPLICATION NUMBER: US/10/479,532

; PRIOR FILING DATE: 2003-12-03

; PRIOR APPLICATION NUMBER: JP 2001-168792

; PRIOR FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 2

; LENGTH: 2799

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (50)..(2311)

US-10-479-532-2

Query Match 80.3%; Score 1839; DB 18; Length 2799;

Best Local Similarity 95.5%; Pred. No. 0;

Matches 1933; Conservative 0; Mismatches 20; Indels 72; Gaps 1;

Qy 265 TTTAGGTACCTGGTTCCTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 324

Db 362 TATTGTACCTGGTTCCTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 421

Qy 325 AAGGGAGACTGACGGCCAAAGGAGGCCCGAAAGTTCTTCCGCAGAGATTGTCTGCGCTG 384

Db 422 AAGGGAGACTGACGGCCAAAGGAGGCCCGAAAGTTCTTCCGCAGAGATTGTCTGCGCTG 481

Qy 385 GACTCTGTCCACAGCTACTCCATCTGCCACAGAGACTTAAGCCCGAGAGACCTGCTTTTG 444

Db 482 GACTCTGTCCACAGCTACTCCATCTGCCACAGAGACTTAAGCCCGAGAGACCTGCTTTTG 541

Qy 445 GATCAGAAAAACAACATCCCATTTGCAGACTTCGGCATGGCGTCCCTGCAGGTGGGGAC 504

Db 542 GATCAGAAAAACAACATCCCATTTGCAGACTTCGGCATGGCGTCCCTGCAGGTGGGGAC 601

Qy 505 AGCTCTGTGAGACCAAGTCCGGTCCCGCATTTATGCGTGTCCAGAGGTGATTAAAGGG 564

Db 602 AGCTCTGTGAGACCAAGTCCGGTCCCGCATTTATGCGTGTCCAGAGGTGATTAAAGGG 661

Qy 565 GAAAAATATGATGCGCGCGGAGACATGTGGAGCTGTGGAGTTCATCTTTCGCGCTG 624

Db 662 GAAAAATATGATGCGCGCGGAGACATGTGGAGCTGTGGAGTTCATCTTTCGCGCTG 721

Qy 625 CTGCTGGGGGCTCTGCGCTTTGATGACACAACTCCCGCAGGTGCTGGAGAGGTGAAA 684

Db 722 CTGCTGGGGGCTCTGCGCTTTGATGACACAACTCCCGCAGGTGCTGGAGAGGTGAAA 781

Qy 685 CGGGGGCTTTTCCATATGCCCCCTTCAATTTCTCCAGATTGCCAGAGCCCTCTGAGGGGA 744

Db 782 CGGGGGCTTTTCCATATGCCCCCTTCAATTTCTCCAGATTGCCAGAGCCCTCTGAGGGGA 841

Qy 745 ATGATCGAAGTGGAGCCCGGAGAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG 804

Db 842 ATGATCGAAGTGGAGCCCGGAGAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG 901

Qy 805 TACTTAGCGGGGAAAACACAGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCGCGGGTA 864

Db 902 TACTTAGCGGGGAAAACACAGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCGCGGGTA 961


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Qy 1068 GAATGATGTTGACCCCGCCGGAAGCGTGTGGATTCTCCCATGCTGAGCCGTCAAGGAA 1127
Db 301 GAATGATGTTGACCCCGCCGGAAGCGTGTGGATTCTCCCATGCTGAGCCGTCAAGGAA 360
Qy 1128 CGCGGACACGAGCGGAGTCCATGGAAGTCTTGGAGATGAGCATACCGATGCGGGGGTGTGG 1187
Db 361 CGCGGACACGAGCGGAGTCCATGGAAGTCTTGGAGATGAGCATACCGATGCGGGGGTGTGG 420
Qy 1188 CTCCGCTGTACCCACCGACCGGCTTGGAGATGAGCATGAGCATGAGCATGAGCATGAGCAT 1247
Db 421 CTCCGCTGTACCCACCGACCGGCTTGGAGATGAGCATGAGCATGAGCATGAGCATGAGCAT 480
Qy 1248 CGTCACTGAGCTTCCAGCGTCTGTCTCTCAGCGCTCTAAGCAGCCCAAGAGTCCGGT 1307
Db 481 CGTCACTGAGCTTCCAGCGTCTGTCTCTCAGCGCTCTAAGCAGCCCAAGAGTCCGGT 540
Qy 1308 CTTTTCTTTTACCGGACCGCGGCTTGGAGATGAGCTCGAGCGGGGCTCCCGAC 1367
Db 541 CTTTTCTTTTACCGGACCGCGGCTTGGAGATGAGCTCGAGCGGGGCTCCCGAC 600
Qy 1368 TTCAAAACGAGAGCTGCTTCTCGGGGCCCCAGAGGCTGAGGAGCGCGGAGAGAGCC 1427
Db 601 TTCCAAAACGAGAGCTGCTTCTCGGGGCCCCAGAGGCTGAGGAGCGCGGAGAGAGCC 660
Qy 1428 CCGCGCCCCAGTCCCGCTCCACACCCCTCCCGGCCCCCAGGCTCCCGCGCTCCTC 1487
Db 661 CCGCGCCCCAGTCCCGCTCCACACCCCTCCCGGCCCCCAGGCTCCCGCGCTCCTC 720
Qy 1488 TGGGGGACCCCTTGCACTCGCTCTGCAACCGCCCGGCGGCTCCACCGGAGACCC 1547
Db 721 TGGGGGACCCCTTGCACTCGCTCTGCAACCGCCCGGCGGCTCCACCGGAGACCC 780
Qy 1548 GGGGACAAACACCCCGCGCGGCTGAGGCTGAGGAGCGCGCTGAGAGAGTCG 1607
Db 781 GGGGACAAACACCCCGCGCGGCTGAGGCTGAGGAGCGCGCTGAGAGAGTCG 840
Qy 1608 TCTCAATCCATCCGACAGCTTCTGGGCTCCCTCGCTTCCACCGGCGAGAGTGA 1667
Db 841 TCTCAATCCATCCGACAGCTTCTGGGCTCCCTCGCTTCCACCGGCGAGAGTGA 900
Qy 1668 GGTCCCTACCGCTGAGGAGTGTCCAGCTTGACCGCAGAGTCTCCCGGAGCTGGCAA 1727
Db 901 GGTCCCTACCGCTGAGGAGTGTCCAGCTTGACCGCAGAGTCTCCCGGAGCTGGCAA 960
Qy 1728 ACCTCTCTGTTGGGAACTTCTCTCTGGAAGAAAGAAACAAATATTTCTCTGCT 1787
Db 961 ACCTCTCTGTTGGGAACTTCTCTCTGGAAGAAAGAAACAAATATTTCTCTGCT 1020
Qy 1788 AAGGACAAACCTCTCAGCAGCATCAAGCAGACATCGTCCATGCTTCTGATGCC 1847
Db 1021 AAGGACAAACCTCTCAGCAGCATCAAGCAGACATCGTCCATGCTTCTGATGCC 1080
Qy 1848 CAGCTGAGTCAAGTGTGCTGTCAACAGCAGCTTCAAGGCGGAGTACAGGCGAGTGG 1907
Db 1081 CAGCTGAGTCAAGTGTGCTGTCAACAGCAGCTTCAAGGCGGAGTACAGGCGAGTGG 1140
Qy 1908 CGGCCCCCTCTTCCAAAAGCCCGTCCGCTTCCAGGTGACATCAGCTCCTCTGAGGG 1967
Db 1141 CGGCCCCCTCTTCCAAAAGCCCGTCCGCTTCCAGGTGACATCAGCTCCTCTGAGGG 1200
Qy 1968 TCCAGAGCCCTCCCGGACCGGACCGGAGGAGTGGGATCTACTCCGTCACCTT 2027
Db 1201 TCCAGAGCCCTCCCGGACCGGACCGGAGGAGTGGGATCTACTCCGTCACCTT 1260
Qy 2028 CACTCTATCTCGGCTCCAGCGTCCGCTTCAAGCGAGTGTGAGACCATCCAGGACCA 2087
Db 1261 CACTCTATCTCGGCTCCAGCGTCCGCTTCAAGCGAGTGTGAGACCATCCAGGACCA 1320
Qy 2088 GCTCTGAGCACTCATGACCGCCCTCTCGTACGCGCTTGGCAGACGAGAAAGACGGGG 2147
Db 1321 GCTCTGAGCACTCATGACCGCCCTCTCGTACGCGCTTGGCAGACGAGAAAGACGGGG 1380
Qy 2148 CCAGACCGGCGCTGCTGTGTCGCCACCCCGGAGCGCTGACGCCCCCAGACCGCGGCCCGCAGA 2207
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Db 1381 CCAGACCGGCGCTGCTGTGTCGCCACCCCGAGCTGAGGCCCCACCCAGCCGCCAGA 1440
Qy 2208 CCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCCCAAGGACAAAGAGTCTCTGGGCAC 2267
Db 1441 CCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCCCAAGGACAAAGAGTCTCTGGGCAC 1500
Qy 2268 CAAGGGACCCCTCTGCGCTGA 2289
Db 1501 CAAGGGACCCCTCTGCGCTGA 1522

RESULT 14
US-10-120-988-221
; Sequence 221, Application US/10120988
; Publication No. US20030219745A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyan
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_fl_genes Version 2.0
; SEQ ID NO 221
; LENGTH: 1797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(1787)
US-10-120-988-221

Query Match 42.8%; Score 980; DB 17; Length 1797;
Best Local Similarity 75.4%; Pred. No. 1.7e-273;
Matches 1470; Conservative 0; Mismatches 0; Indels 480; Gaps 1;

Qy 268 AGGTACCTGTTCTGGAGCAGCTCTCGGGGGTGGAGTATTCGACTACCTGGTAAAGAG 327
Db 87 AGGTACCTGTTCTGGAGCAGCTCTCGGGGGTGGAGTATTCGACTACCTGGTAAAGAG 146
Qy 328 GGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGCGCAGATTTGTCTGCGCTGGAC 387
Db 147 GGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGCGCAGATTTGTCTGCGCTGGAC 206
Qy 388 TTCTGCCACAGCTACTCCATCTGCCACAGAGCCTTAAGCCCGAGAACCTGCTTTTGAT 447
Db 207 TTCTGCCACAGCTACTCCATCTGCCACAGAGCCTTAAGCCCGAGAACCTGCTTTTGAT 266
Qy 448 GAGAAAAACAATCCCGCATTTGAGACTTCGGCATGCGCTCCCTGCGAGGTGGGACAGC 507
Db 267 GAGAAAAACAATCCCGCATTTGAGACTTCGGCATGCGCTCCCTGCGAGGTGGGACAGC 326
Qy 508 CTCTGTGAGACCAAGCTCGGGTCCCCCAATATGCTGTTCAGAGGTGATTAAGGGGAA 567
Db 327 CTCTGTGAGACCAAGCTCGGGTCCCCCAATATGCTGTTCAGAGGTGATTAAGGGGAA 386
Qy 568 AATATATATGCGCGCCGCGAGCATGTGGAGCTGGAGTCACTCTTTCGCCCTGCTC 627
Db 387 AATATATGCGCGCCGCGAGCATGTGGAGCTGGAGTCACTCTTTCGCCCTGCTC 446
Qy 628 GTGGGGGCTCTGCCCTTTTGTAGTACGACAACTCCGCGCAGCTGCTGGAGAGTGAACGG 687
Db 447 GTGGGGGCTCTGCCCTTTTGTAGTACGACAACTCCGCGCAGCTGCTGGAGAGTGAACGG 506
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QY	688	GGGCTCTTCCACATGCCCACTTCAATTCCTCCAGATTGCGAGGCTCTCGAGGGAATG	747
Db	507	GGCGTCTTCCACATGCCCACTTCAATTCCTCCAGATTGCGAGGCTCTCGAGGGAATG	566
QY	748	ATCGAAGTGAGCGCGGAAAGAGCTCAGTCTGGAGCAAAATTCAGAAAATCCTTGGTAC	807
Db	567	ATCGAAGTGAGCGCGGAAAGAGCTCAGTCTGGAGCAAAATTCAGAAAATCCTTGGTAC	626
QY	808	CTAGCGGGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTCGCCCGCGGTAGCC	867
Db	627	CTAGCGGGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTCGCCCGCGGTAGCC	686
QY	868	ATGCGGAGCCTGCGCATCAACGAGAGCTGGACCCCGACGCTCTAGAGAGCATGGCATCA	927
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QY	928	CTGGGCTGCTTCAGGACCCGAGAGCTGCATCGCGAGCTGCGCAGTGGAGGAGGAAAC	987
Db	747	CTGGGCTGCTTCAGGACCCGAGAGCTGCATCGCGAGCTGCGCAGTGGAGGAGGAAAC	806
QY	988	CAAGAAAAGATGATATATATATCTCTTTTGGATCGGAAGAGCGGTATCCAGCTGTGAG	1047
Db	807	CAAGAAAAGATGATATATATCTCTTTTGGATCGGAAGAGCGGTATCCAGCTGTGAG	866
QY	1048	GACAGGACCTGCTCCCGGAAATGATTTGACCCCGGAGCGCTGCGGAGCGGTGGAATCTCCC	1107
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QY	1108	ATGCTGAGCCGTACGCGGAAGCGGCGACGAGCGGAAGTCCATGGAAGTCTTGAGCATC	1167
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QY	1168	ACCGATGCGGGGGTGGTCCCTGTACCCACCGGCGGCTTGGAGTGGCCCGAG	1227
Db	987	ACCGATGCGGGGGTGGTCCCTGTACCCACCGGCGGCTTGGAGTGGCCCGAG	1046
QY	1228	CACAGCCAGATCCCGTAGCGTCAGTGGAGCCTCCACGGGTCTGTCTCCAGCCCTCTA	1287
Db	1047	CACAGCCAGATCCCGTAGCGTCAGTGGAGCCTCCACGGGTCTGTCTCCAGCCCTCTA	1057
QY	1288	AGCAGCCCAAGAGTCCGCTCTTTTTCACCGGAGCGGGGGCTGGAGATGAGGCT	1347
Db	1058	AGCAGCCCAAGAGTCCGCTCTTTTTCACCGGAGCGGGGGCTGGAGATGAGGCT	1057
QY	1348	CGAGGGGGGGTCCCGGACTTCCAAAGCAGAGCTGCTCTCTCGGGGCCCGAGGGT	1407
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QY	1408	GGGGGGCGGGGAGCAGCCCGCCCGCCAGTGCCTCCAGTCCACACCCTGCGCGGCCCC	1467
Db	1058	GGGGGGCGGGGAGCAGCCCGCCCGCCAGTGCCTCCAGTCCACACCCTGCGCGGCCCC	1057
QY	1468	CCAGGCTCCCGGGCTCTCTGGGGGAGCCCTTTCAGTCTGCGCTCTGCACAGCCCGG	1527
Db	1058	CCAGGCTCCCGGGCTCTCTGGGGGAGCCCTTTCAGTCTGCGCTCTGCACAGCCCGG	1057
QY	1528	GCCAGTCCACCGGAGCCCGGGGCAACACACCCCGAGCCCGGGGGTGGCGTCCGG	1587
Db	1058	GCCAGTCCACCGGAGCCCGGGGCAACACACCCCGAGCCCGGGGGTGGCGTCCGG	1057
QY	1588	GGAGCGCCCTGGAGAGTCTCTCAACTCCGCTGAGAGATGTCAGTCTGACGCCAGAG	1647
Db	1058	GGAGCGCCCTGGAGAGTCTCTCAACTCCGCTGAGAGATGTCAGTCTGACGCCAGAG	1057
QY	1648	TTTTCACCGGCGAAGATGAGGTCCTTACCGCTGAGAGATGTCAGTCTGACGCCAGAG	1707
Db	1058	TTTTCACCGGCGAAGATGAGGTCCTTACCGCTGAGAGATGTCAGTCTGACGCCAGAG	1057
QY	1708	TCCTCCCGGAGCTGGCAAAACGCTCTGTTTGGGAACTTCACTCTCTTGGAGCAAGAA	1767
Db	1058	TCCTCCCGGAGCTGGCAAAACGCTCTGTTTGGGAACTTCACTCTCTTGGAGCAAGAA	1106
QY	1768	GAACAAATATTCCTCGTCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATCGTC	1827

Db	1107	GAACAAATATTCCTCGTCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATCGTC	1166
QY	1828	CATGCTTTCTGTGATCCCGAGCTCAGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1887
Db	1167	CATGCTTTCTGTGATCCCGAGCTCAGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1226
QY	1888	GCCAGGTACAAAGGACAGTGGCGGCCCTCTCGTCTTCCAAAGGCCGCTCGGTTCAGGTG	1947
Db	1227	GCCAGGTACAAAGGACAGTGGCGGCCCTCTCGTCTTCCAAAGGCCGCTCGGTTCAGGTG	1286
QY	1948	GACATCAGCTCCTGTAGGCTCCAGAGCCCTCCCGGAGCGGACGCGAGGAGGTGGT	2007
Db	1287	GACATCAGCTCCTGTAGGCTCCAGAGCCCTCCCGGAGCGGACGCGAGGAGGTGGT	1346
QY	2008	GGCATCTACTCCGTCACTCTCTCATCTCGGGTCCAGCCCTCGGTTCAGCGAGTG	2067
Db	1347	GGCATCTACTCCGTCACTCTCTCATCTCGGGTCCAGCCCTCGGTTCAGCGAGTG	1406
QY	2068	GTGGAGACCATCCAGGCAAGCTCTGTAGCACTCATATGACAGCCCTCGGTTCAGGCTTG	2127
Db	1407	GTGGAGACCATCCAGGCAAGCTCTGTAGCACTCATATGACAGCCCTCGGTTCAGGCTTG	1466
QY	2128	GCAGAGAGAAACGCGGCCCGAGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2187
Db	1467	GCAGAGAGAAACGCGGCCCGAGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1526
QY	2188	CCCCACCCCGCGGCCCGAGCCAGAGCTG	2217
Db	1527	CCCCACCCCGCGGCCCGAGCCAGAGCTG	1556

RESULT 15
US-10-283-247-4
; Sequence 4, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:

; APPLICANT: NEELAW, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1911
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-283-247-4

Query Match 35.0%; Score 800.8; DB 15; Length 1911;
Best Local Similarity 68.4%; Pred. No. 1.7e-221; Indels 129; Gaps 7;
Matches 1277; Conservative 0; Mismatches 462;

QY	265	TTTAGTACCTCTGTTCTGGAGCAGCTCTCGGGGGTGGAGCTATTTCGATCTACCTGGTAAAG	324
Db	88	TATTTGTACCTCTGTTCTGGAGCAGCTCTCGGGGGTGGAGCTATTTCGATCTACCTGGTAAAG	147
QY	325	AAGGGAGACTGACGCCCAAGAGGCGCCGAAAGTTCTTCGCCAGATTGTCTGCGCTG	384
Db	148	AAGGGAGGCTGACGCCCAAGAGGCGCTCGGAAAGTTCTTCGCCAGATTGTCTGCGCTG	207
QY	395	GACTTCTGCCACAGCTACTCTCCATCTGCCAGAGACCTAAAGCCCGAGAACCTGCTTTTG	444
Db	208	GACTTCTGCCACAGCTACTCTCCATATGCCACAGGATCTGAAACCTGAAACCTCTCTG	267
QY	445	GATGAGAAAAACATCCCGCATTCGAGACTTCGCGATGGCGTCCCTGCGAGTGGGGAC	504
Db	268	GACGAGAGAACATCCCGCATTCGAGACTTCGCGATGGCGTCCCTGCGAGTGGGGAC	327
QY	505	AGCTCTCTGGAGACAGCTGCGGGTCCCGCCCATTTATGCGTGTCCAGAGGTGATTAAAGGG	564

328	Db		AGCCTGTTGGAGACAGCTGTGGGTGCCCCCACTACGCTTCCGCCGAGGTGATCCGGGGG	387
565	Qy	GA AAAATATGATGTCGCGGCGAGACATGTGGAGCTGTGAGTCATCTCTTCGCGCCCTG	624	
388	Db	GAGAA GTATGACGCGCGGAAGCGGACGTGTGAGCTGCGGCGTATCTCTGTTGCGCTTG	447	
625	Qy	CTCGTGGGGCTCTGCCCTTTTGATGACGACAACTCCGCCACGCTGCTGGAGAAAGTGA	684	
448	Db	CTGTGGGGGCTCTGCCCTTCGACGATGACAACTTCGACAGCTGCTGGAGAAGTGAAG	507	
685	Qy	CGGGGCGTCTTCACATGCCCCACTTCATTTCTCTCAGATTGCCAGAGCTCTCTGAGGGGA	744	
508	Db	CGGGGCGTGTTCACATGCCGCACTTTATCCGCGCGACTGCTCCAGAGTCTGCTACGGGGC	567	
745	Qy	ATGATCGAAGTGGAGCCGGA AAAAGGCTCAGTCTGAGCAAAATTCAGAAACATCTCTTG	804	
568	Db	ATGATCGAGGTGAGCGCGCACGCGCGCTCAGCTAGAGACATTCAGAAACACATATGG	627	
805	Qy	TACCTAGCGGGAAACAGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCGCGGGTA	864	
628	Db	TATATAGGGGCAAGAAATGAGCCGGAAC-----AGAGCAGCCCATTCCTCGCAAGGTG	681	
865	Qy	GCCATGCGGAGCTGCCATCCAACGGAGAGCTGACCCCGACGCTCTAGAGAGCATGCGCA	924	
682	Db	CAGATCCGCTCGTCTGCCCGAGCTGTGGAGGACATCGACCCGACGTCGTGGACAGCATC	741	
925	Qy	TCACTGGGCTGCTTCAGGGACCGGAGAGGCTGATCGCAGCTGCGCAGTGAGGAGGAG	984	
742	Db	TCACTGGGCTGCTTCCGAGACCGCAACAGCTGCTGCAGGACCTGCTGTCGAGGAGGAG	801	
985	Qy	AACCAAGAAAAGATGATATATTCTCTCTTTGGATCGGAAGGAGCGGTATCCAGTGT	1044	
802	Db	AACAGGAGAAGATGATTACTTCTCTCTCTGACCGGGAAGAAAGTACCCGAGCAG	861	
1045	Qy	GAGGACAGGACTGCTCTCCCGGAATGATGTTGACCCCTCCGGAAGCGTGTGGAATCT	1104	
862	Db	GAGGATGAGGACCTGCCCCCGGAACGAGATAGACCTCTCCCGGAAGCGTGTGGAATCC	921	
1105	Qy	CCCATGCTGAGCCGTACGSGAAGCGGCGCACAGAGCGGAAGTCCATGGAAGTCTTGAC	1164	
922	Db	CCGATGCTGAACCGGACAGGCAAGCGGCGGCAGAACGCAATCCATGGAAGTGTCTCAG	981	
1165	Qy	ATCACCGATGCGGGGGTGGTGCTCCCTGTATCCCAACCGACGGGCTTTGGAGATGCC	1224	
982	Db	GTGAC-----GGACGCGGCTCCCCGCTGCTCGCGGGGGCCATTGAGATGCC	1032	
1225	Qy	CAGCACAGCCAGATCCGTAGCGTCA GTGAGGACCTCAGCGGCTGTCTCTCAGCGCTT	1284	
1033	Db	CAGCACGGCCAGAGTAAAGCAATGTTCA GTA AAAAGCCTGGATATCGCTGAGGCCATCC	1092	
1285	Qy	CTAAGCAGCCCAAGGAGTCCGGTCTTTTCTTTTTCACCGGAGCGGGGCTGGAGATGAG	1344	
1093	Db	CAATTTCAGCA-AAGAACAGGTTCT-----qGTC	1121	
1345	Qy	GCTCGAGCGGGGGCTCCCGACTTCA AAAACGACAGCGTTCCTCTCGGGGGCCCGAGG	1404	
1122	Db	CATCAGCGGTGCTCTCTCAGGCTTTTCCACGAGCCCACTCAGCAGCCCCGGGTGACCCC	1181	
1405	Qy	GTGCGGGGCGCGGGGAGCAGCCCCCGCGCCCGCAGTCCCGCTCCACACCCCTGCCCCG	1464	
1182	Db	TCACCCCTCACAGGGGCGATCCCTCCCG-----	1212	
1465	Qy	CCCCAGGCTCCCGCGCTCTCTCTGCGGGAGCCCTTGTCACTCGCCTCTGCA CAGGCC	1524	
1213	Db	-----ACCCCAAGGGGACACTGTGTCACAGCCCA	1242	
1525	Qy	CGGGCCAGTCCCAACCGGGAACCCCGGGACAAACACACCCCGCCCGCGGTGGCGTC	1584	
1243	Db	AAGGAGAGCCCGGTGGCAAGCCCAACCCCGCGCCCGTCCAGCCCC-----AGGTC	1296	
1585	Qy	GGGGAGCCGCTGAGAGGTGTTCTCAATCTCAATCGCAACAGTCTCTGGGCTCCCT	1644	

Db	1297	GGAGGGGTGCCCTGSGAGGGCGGGCTCAACTCCATCAAGAAACAGACTTCTTGGGCTCACCC	1356
Qy	1645	CGCTTTACCGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCCAGCTGTGACGCCA	1704
Db	1357	CGCTTCCACCGCGGAAACTGCAAGTTCGAGCGCGGAGGAGATGCCAACTGTGACCA	1416
Qy	1705	GAGTCTCTCCCGGAGCTGGCAAAACGCTCCTGGTTTCGGAACTTTCATCTCTTGGACAAA	1764
Db	1417	GAGTCGTGCTCCCAAGCTGGCGAAGAGTCTCTGGTTTGGGAACTTTCATCAGCCTCGGAGAAG	1476
Qy	1765	GAGAGCAAAATATTCCTGCTGCTTAAGGACAAACCTCTCAGCAGACNTCAAAGCAGACATC	1824
Db	1477	GAGGAGCAGATCTTCGTGGTTCATCAAGAACAACTCTCAGCTGCCATCAAGGCTGACATC	1536
Qy	1825	GTCCATGSCCTTCTGTGCAATCCCAAGCTTCAGTGTGTCACAGTGTGTCACAGACCAAGCTTC	1884
Db	1537	GTGCAAGCCTTCTGTGCAATCCAGTCTCAGCCACAGCTCATCTCCCAACGAGCTTTC	1596
Qy	1885	AGGGCCGAGTACAAGGCCAAGTGCGGCGCCCTCCGTCTTCCAAAAGCCCGTCCGCTTCCAG	1944
Db	1597	CGGGCCGAGTACAAGGCCACGGGGGGCCAGCGGTGTTCCAGAGACCGGTCAAGTTCAG	1656
Qy	1945	GTGCAATCAGCTCTCTGAGGGTTCAGAGCCCTCCCCCGACAGGAGCGGACGGAGGT	2004
Db	1657	GTTGATATCACCTACACGGAGGT-----GGGGAGCGCAGAGGAG	1698
Qy	2005	GTTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCGCTCGGTTCAAGCGA	2064
Db	1699	AACGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCGCTCGGTTCAAGAGG	1758
Qy	2065	GTGTTGGAGACCATCCAGGCACAGCTCTTGAAGCACTCATGACAGCCCTTCGTTGACGGCC	2124
Db	1759	GTGTTGGAGACCATCAGGCCAGCTGCTGAGCACACAGACCCGCTCGGCGCCAGCAC	1818
Qy	2125	CTGGCAGA	2132
Db	1819	TTGTGAGA	1826

Search completed: February 19, 2005, 17:04:03
Job time : 1219 secs

— This Page Blank (uspto)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 08:09:53 ; Search time 9587 Seconds
(without alignments)
11569.207 Million cell updates

Title: US-10-803-277-3

Perfect score: 2289

Sequence: 1 atgggacttgagtttggttt.....acgggaccctctgccctga 2289

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs. 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Minimum DB seq	length: 0
Maximum DB seq	length: 2000000000

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%

Maximum value 100%
Listing first 45 summaries

Database :

GenEmbl: ★

1: qb ba:★

2: gbhta: *

3: gb_in:*

4: gb_om: *

4: qb_om: ★
5: qb_ov: ★

6. qib-mat: *

6: gb_pa: *

7. a. $\frac{1}{2}$ b. $\frac{1}{2}$ c. $\frac{1}{2}$

*:१५
*:३

9: gb pr:*

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10: gb_ro:
11: gb_ro:
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11: gb_stb:
12: gb_stb: *
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12: gb_sy: *
13: gb_sy: *
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13: gb_un: *
14: gb_un: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result	No.	Score	Query		DB	ID	Description		
			Match	Length					
1	2020.2	88.3	2385	6	AX166526	Sequence	AX166526	Sequence	
2	2020.2	88.3	2576	6	BD185210	Novel gen	BD185210	Novel gen	
3	2020.2	88.3	2576	6	AB058714	Homo sapi	AB058714	Homo sapi	
4	2020.2	88.3	2870	9	AY458602	Homo sapi	AY458602	Homo sapi	
5	2020.2	88.3	2897	6	AX642966	Sequence	AX642966	Sequence	
6	2020.2	88.3	3007	9	AF479826	Homo sapi	AF479826	Homo sapi	
7	2020.2	88.3	3109	9	AF479827	Homo sapi	AF479827	Homo sapi	
8	1839	80.3	2799	6	BD186023	Cell cycl	BD186023	Cell cycl	
9	1727.8	75.5	2331	10	AY536671	Mus muscu	AY536671	Mus muscu	
10	1510.4	66.0	1902	6	CQ841950	Sequence	CQ841950	Sequence	
11	1510.4	66.0	1902	9	AX124999	Homo sapi	AX124999	Homo sapi	
12	1473.6	64.4	2128	9	BC016681	Homo sapi	BC016681	Homo sapi	
13	1033.2	45.1	1623	6	CO727250	Sequence	CO727250	Sequence	
14	980	42.8	1797	6	AR541973	Sequence	AR541973	Sequence	
15	780.4	34.1	3364	6	AR232171	Sequence	AR232171	Sequence	
16	778.8	34.0	2308	6	AR232170	Sequence	AR232170	Sequence	
17	777.2	34.0	1827	6	AX661193	Sequence	AX661193	Sequence	
18	777.2	34.0	2007	6	AX661191	Sequence	AX661191	Sequence	
19	777.2	34.0	2647	6	AX766346	Sequence	AX766346	Sequence	

20	777.2	34.0	3576	9	AK131534	AK131534	Homo sapi
21	776	33.9	4133	10	AK173268	Mus muscu	
22	775.6	33.9	3117	9	AF533876	Homo sapi	
23	775.6	33.9	3516	9	AY166857	Homo sapi	
24	775.6	33.9	3586	9	AF533879	Homo sapi	
25	773.2	33.8	1956	9	HSAG701	Homo sapi	
26	773.2	33.8	2025	6	AK327995	Sequence	
27	773.2	33.8	2025	6	AK750714	Sequence	
28	773.2	33.8	2219	6	AK327993	Sequence	
29	773.2	33.8	3164	9	AF533877	Homo sapi	
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31	773.2	33.8	3532	9	AK122851	Homo sapi	
32	773.2	33.8	4888	9	AF533878	Homo sapi	
33	772.8	33.8	2160	10	AY533674	Mus muscu	
34	772.6	33.8	4055	10	AY560739	Mus muscu	
35	770.4	33.7	2028	10	AY533673	Mus muscu	
36	769.4	33.6	1962	10	AY533672	Mus muscu	
37	690	30.1	3342	10	BC056498	Mus muscu	
38	541	23.6	1014	9	HSM803233		
39	491.8	21.5	3156	9	AK074411	Homo sapi	
40	463.8	20.3	1115	6	CQ731316	Sequence	
41	408.4	17.8	38000	9	AC008974	Homo sapi	
42	371	16.2	134793	9	AC020922	Homo sapi	
43	337.2	14.7	2720	6	CQ585216	Sequence	
44	337.2	14.7	5609	3	AY060288	Drosophil	
45	315.2	13.8	226060	2	AC079583	Mus muscu	

ALIGNMENTS

RESULT 1			
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LOCUS			
DEFINITION	Sequence 17 from Patent WO0138503.		
ACCESSION	AXI166526		
VERSION	AXI166526.1 GI:14546871		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R., Flanagan,P. and Clardy,D.S. Novel human protein kinases and protein kinase-like enzymes Patent: WO 0138503-A 17 31-MAY-2001;		
JOURNAL	Sugen, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1..2385 organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon.9606"		

ORIGIN	Query Match	88.3%	Score 2020.2;	DB 6;	Length 2385;
	Best Local Similarity	99.9%;	Pred. No. 0;		
	Matches 2022;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	265	TTTATGGTACCTGGTTCTTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTTAAAG	324		
Db	361	TATTTGTACCTGGTTCTTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTTAAAG	420		
Qy	325	AAGGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGCCCAGATGTGTCTCGCGCTG	384		
Db	421	AAGGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGCCCAGATGTGTCTCGCGCTG	480		
Qy	385	GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG	444		
Db	481	GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG	540		
Qy	445	GATGAGAAAAACAACATCCGCATTGCGACTTCGGCATGGCGTCCCTCGCAGGTGGGGGAC	504		

541 GATGAGAAAAACAATCCGCAATTCGAGACTTCGGCATGGCGTCCCTGCAGGTGGGSEAC 600
 505 AGCTCTCTGAGACCAAGTCCGGGTCCCCCAATATGCGTGTCCAGAGGTGATTAAAGGGG 564
 601 AGCTCTCTGAGACCAAGTCCGGGTCCCCCAATATATGCGTGTCCAGAGGTGATTAAAGGGG 660
 565 GAAAAATATGATGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCAATCTCTTCGCCCTG 624
 661 GAAAAATATGATGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCAATCTCTTCGCCCTG 720
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 721 CTGCTGGGGGCTCTGCCCTTTGATGACGACAACTCCGCGAGCTGTGGAGAGGTGAAA 780
 685 CGGGGCTCTTCCATGCCCCCACTTCAATCTCTCAGATTCGAGAGCTCTCTGAGGGA 744
 781 CGGGGCTCTTCCATGCCCCCACTTCAATCTCTCAGATTCGAGAGCTCTCTGAGGGA 840
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 805 TACCTAGCGGGAACACAGAGCAGACCCGCTGCTGAGGAGCCCTGCGCGCGGGTA 864
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 865 GCCATGCGAGCGCTGCCATCCAAACGAGAGTGCATCGCGAGCTGCGCAGTGGAGGAG 924
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 1801 GAGTCTCCCGGAGCTGGCAAAACGCTCTCTGTTTCGGGAACTTCACTCTCTTGGACAAA 1860
 1765 GAAGAACAAATATTTCTCTGCTTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1824
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 1921 GTCCATGCTTCTCTGCTGATCCCGAGCTGAGTCAAGTGTGTGTCAAGACAGCTTTC 1980
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 2245 AAGGACAAAGAGTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2289
 2341 AAGGACAAAGAGTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2395

RESULT 2
 BD185210 2576 bp DNA linear PAT 17-JUN-2003
 LOCUS Novel genes and proteins encoded by the genes.

DEFINITION Novel genes and proteins encoded by the genes.
 ACCESSION BD185210
 VERSION BD185210.1 GI:31877410
 KEYWORDS JP 2002345493-A/53
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 Ohara O., Nagase, T. and Nakajima, D.
 Novel genes and proteins encoded by the genes
 Patent: JP 2002345493-A 53 03-DEC-2002;

JOURNAL KAZUSA DNA RESEARCH INSTITUTE
 COMMENT OS Homo sapiens (human)
 PN JP 2002345493-A/53
 PD 03-DEC-2002

PF 26-FEB-2002 JP 2002049046
 PI OSMU OHARA, TAKAHIRO NAGASE, DAISUKE NAKAJIMA
 PC C12N15/09, C07K14/47, C07K14/54, C12N15/00
 CC Novel genes and proteins encoded by the genes FH Key

FEATURES		Location/Qualifiers		Query Match	
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ACCESSION	AB058714						
VERSION	AB058714.1	GI:14017838					
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ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
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TITLE	1 (sites)						
JOURNAL	Nagase, T., Nakayama, M., Nakajima, D., Kikuno, R. and Ohara, O.						
MEDLINE	Prediction of the coding sequences of unidentified human genes. XX.						
PUBMED	The complete sequences of 100 new cDNA clones from brain which code						
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LOCUS Sequence 43 from Patent WO0109547.
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ACCESSION AX642966
VERSION AX642966.1 GI:28550113
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Yue H., Lal, P., Bandman, O., Borowsky, M., Au-Young, J., Lu, Y.,
Gandhi, A.R., Tribouley, C.M., Walla, N., Yao, M.G., Lu, D.A.,
Greenwald, S.R., Ramkumar, J., Griffin, J.A., Kearney, L., Burford, N.,
Nguyen, D.B., Tang, Y.T., Baughn, M.R., He, A., Thornton, M.,
Hafalia, A., Patterson, C., Gururajan, R., Lo, T.P., Khan, F.,
Recipon, S.A., Azimzai, Y., Policky, J.L., Ding, L., Grether, M.,
Elliot, V.S., Thangavelu, K., Batra, S. and Ison, C.H.
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TITLE Patent: WO 0109547-A 43 20-DEC-2001;
JOURNAL Inocyte Genomics, Inc. (US)
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ACCESSION AF479827
VERSION AF479827.1 GI:19401873

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
She,X.Y., Yu,L. and Guo,J.H.

REFERENCE

1 (bases 1 to 3109)
Direct Submission
Submitted (02-FEB-2002) School of Life Sciences, Laboratory of
Human Genes Research, Institute of Genetics, Fudan University, 220
Handan Road, Shanghai 200433, P. R. China

FEATURES

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RESULT 9
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LOCUS
DEFINITION Mus musculus putative serine/threonine kinase SADB mRNA, complete cds.
ACCESSION AY533671
VERSION AY533671.1 GI:47013800
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2331)
AUTHORS Kishi, M. and Sanes, J. R.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2004) Department of Anatomy and Neurobiology, Washington University School of Medicine, 660 South Euclid, St. Louis, MO 63110, USA

FEATURES
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ORIGIN
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Best Local Similarity 91.0%; Pred. No. 0;
Matches 1837; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
Qy 271 TACTGCTTCTGAGCAGCTCTCGGGGGTGGAGCTATTTCGACTACCTGGTAAAGAAGGG 330
Db 313 TACTTGGTCTTGGACAGCTTCTGGTGGTGGAGCTGTTCCACTACCTGGTAAAGAAGGG 372

Isogai, T. and Yamamoto, J.		Takao Isogai, FLJ Project (HRI Team); 2-6-7	
Direct Submission		Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7	
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan		(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)	
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.		Location/Qualifiers	
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QY	838	CTGAGCAGCCCTGCGCGCGGTAGCCATCGGAGCTGCCATCCAAACGAGAGCTG	897
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QY	898	GACCCGACGCTCTTAGAGAGCATGGCATCACTGGCTGCTTCAAGGACCGCGAGAGCTG	957
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QY	958	CATCGGAGCTGCCAGTGGAGGAGAACCAAGAAAGATGATATATTCTGCTTTTG	1017
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DB	312	GATCGGAAGGAGCGGTATCCAGCTGTGAGGACCAAGACCTGCTCCCGGAATGATGTT	371
QY	1078	GACCCCGCGGAAGCGGTGATTTCTCCATGCTGAGCGGTCAACGGGAAGCGCGACCA	1137
DB	372	GACCCCGCGGAAGCGGTGATTTCTCCATGCTGAGCGGTCAACGGGAAGCGCGACCA	431
QY	1138	GAGCGGAAGTCCATGGAAGTCTGAGCATCACCGATGCGGGGTGGTGGCTCCCTGTA	1197
DB	432	GAGCGGAAGTCCATGGAAGTCTGAGCATCACCGATGCGGGGTGGTGGCTCCCTGTA	491
QY	1198	CCACCCGAGCGGCTTGGAGATGGCCAGCAGCAGATCCCTAGCGTCAGTGA	1257
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QY	1258	GCCTCCACGGGTGTCTCCAGCCCTTAAGCAGCCCAAGAGTCCCGTCTTTTCTTTT	1317
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QY	1318	TCACCGGAGCCGGGGCTGGAGATGAGGCTCGAGCGGGGGCTCCCGACTTCCAAAACG	1377
DB	612	TCACCGGAGCCGGGGCTGGAGATGAGGCTCGAGCGGGGGCTCCCGACTTCCAAAACG	671
QY	1378	CAGACGCTGCTTCTCGGGGCGCCAGAGGTGGGGCGCGGGGAGCAGCCCGCCCGCC	1437
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732	AGTGCCCGCTCCACACCCCTGCGCGCGCCCCCAGAGTCTCCCGCGCTCTCTCTGCGGGGACC	791	
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DB	792	CCCTTTGCACTCCGCTCTTGACACACGCCCCCGGGCCAGTCCCAACCGGGACCCCGGGGACAACA	851
QY	1558	CCACCCCGCAGCCCGCGGGTGGCTGCGGGGAGCGCCCTGGAGGAGTGTCTCTCAACTCC	1617
DB	852	CCACCCCGCAGCCCGCGGGTGGCTGCGGGGAGCGCCCTGGAGGAGTGTCTCTCAACTCC	911
QY	1618	ATCCGCAACAGCTTCTTGGGCTCCCTCGCTTTTTCACCGCGCAAGATGACAGTCCCTTACC	1677
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DB	1032	TTCCGGGAATTCATCTCTCTTGGAACAAAGAAACAAATATTTCTCTGCTTAAAGGACAAC	1091
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DB	1092	CCTCTCAGCAGCATCAAGACGACATCGTCCATGCTTCTTGTGTCATCCCGAGCTCTGAGT	1151
QY	1858	CACAGTGTGCTGTACAGACCAAGCTTTCAGGCGCGAGTACAAAGGCCAGTGGCGGCCCTCC	1917
DB	1152	CACAGTGTGCTGTACAGACCAAGCTTTCAGGCGCGAGTACAAAGGCCAGTGGCGGCCCTCC	1211
QY	1918	GTCTTCCAAAAGCGCTCCGCTTCCAGGTGGACATCAGCTCTCTGAGGGTCCAGAGCCC	1977
DB	1212	GTCTTCCAAAAGCGCTCCGCTTCCAGGTGGACATCAGCTCTCTGAGGGTCCAGAGCCC	1271
QY	1978	TTCCCGGAGCGGACCGCGAGGTGGTGGCATCTACTCCGTCACCTTCACTCTCATC	2037
DB	1272	TTCCCGGAGCGGACCGCGAGGTGGTGGCATCTACTCCGTCACCTTCACTCTCATC	1331
QY	2038	TTGGGTCCCGACCGCTCGGTTTCAAGCGAGTGGTGGAGACCATCCAGGCAAGCTCTTGA	2097
DB	1332	TTGGGTCCCGACCGCTCGGTTTCAAGCGAGTGGTGGAGACCATCCAGGCAAGCTCTTGA	1391
QY	2098	ACTCATGACAGCCCTTCCGTCGAGGCGCTGGCAGACGAGAACCGGGGCGGAGCCCGG	2157
DB	1392	ACTCATGACAGCCCTTCCGTCGATGCTTGGCAGACGAGAACCGGGGCGGAGCCCGG	1451
QY	2158	CCTGCTGGTGGCCCCACCCGGAAGCTTCAGCGCCCCCACCCCGGCGCCAGAGAGCTG	2217
DB	1452	CCTGCTGGTGGCCCCACCCGGAAGCTTCAGCGCCCCCACCCCGGCGCCAGAGAGCTG	1511
QY	2218	AGCAGCTTCTCCCGCGGAGGCCCGCCCAAGGACAAAGAGTCTCTGGGCCCAACCGGACC	2277
DB	1512	AGCAGCTTCTCCCGCGGAGGCCCGCCCAAGGACAAAGAGTCTCTGGGCCCAACCGGACC	1571
QY	2278	CCTCTGCCCTGA	2289
DB	1572	CCTCTGCCCTGA	1583
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LOCUS			
DEFINITION			
Homo sapiens KIAA1811 protein, mRNA (cdna clone MGC:21870			
IMAGE:4341838), complete cds.			
ACCESSION			
BC016681			
VERSION			
BC016681.1			
GI:16741775			
KEYWORDS			
MGC.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 2128)			

RESULT 12
BC016681
LOCUS
DEFINITION
Homo sapiens KIAA1811 protein, mRNA (cDNA clone MGC:21870
IMAGE:4341838), complete cds.
ACCESSION
BC016681
VERSION
BC016681.1
KEYWORDS
GI:16741775
SOURCE
MGC.
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2128)

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QY	1830	TGCTTTCTGCTGATCCCCAGCCTGAGTCAAGTGTGCTGTACAGACAGCTTCAGGGC	1889	Db	287	-----AGACCTAAAGCCCGAGAACCTGCTTTTG	314	
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QY	1890	CGAGTACAAAGCCAGTGGCGCCCTCCGCTTTCCAAAGCCCGTCCGCTTCAGGTGA	1949	Db	315	GATGAGAAAAACAACATCCGCAITTCGAGACTTCGGCATGGGCTCCCTGCGAGTGGGGAC	374	
Db	1249	CGAGTACAAAGCCAGTGGCGCCCTCCGCTTTCCAAAGCCCGTCCGCTTCAGGTGA	1308	QY	505	AGCTCTCTGAGAGACAGCTGGCGGTCCCCCATTTATGCGTTCAGAGGTGATTAAGGG	564	
QY	1950	CATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGCAGCGGACGGGAGGTGGTGG	2009	Db	375	AGCTCTCTGAGAGACAGCTGGCGGTCCCCCATTTATGCGTTCAGAGGTGATTAAGGG	434	
Db	1309	CATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGCAGCGGACGGGAGGTGGTGG	1368	QY	565	GAAAAATATGATGGCGCGCGGAGACATGTGGAGCTGTGGAGTCACTCTTTCGCCCTG	624	
QY	2010	CATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGGTTCAGCGAGTGT	2069	Db	435	GAAAAATATGATGGCGCGCGGAGACATGTGGAGCTGTGGAGTCACTCTTTCGCCCTG	494	
Db	1369	CATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGGTTCAGCGAGTGT	1428	QY	625	CTCGTGGGGCTCTGCCCCCTTTGATGACGACAACTCCGCCAGCTGCTTGGAGAGGTGAAA	684	
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Db	1429	GGAGACCATCAGGCAAGTCTCTGAGCACTCATGACCAAGCCCTCCGTCGAGGCCCTGGC	1488	QY	685	CGGGCGCTCTTCCACATGCCACCTTCACTCTCCAGATTGCCAGAGCTCTCTGAGGGGA	744	
QY	2130	AGACGAGAAAGACGGGGCCAGACCCGGCTGCTGTGTCGCCACCCCGAAGCCCTGCAGCC	2189	Db	555	CGGGCGCTCTTCCACATGCCACCTTCACTCTCCAGATTGCCAGAGCTCTCTGAGGGGA	614	
Db	1489	AGACGAGAAAGACGGGGCCAGACCCGGCTGCTGTGTCGCCACCCCGAAGCCCTGCAGCC	1548	QY	745	ATGATCGAAGTGGAGCCCGAAAAAAGGCTCAGTCTTGGAA---GCAAAATTCAGAAACATCTCT	801	
QY	2190	CCCAACCGCGCCGAGACCCAGAGCTGAGCAGCTCTCCCGCGAGGCCCCCGCAAGGA	2249	Db	615	ATGATCGAAGTGGAGCCCGAAAAAAGGCTCAGTCTTGGAA---GCAAAATTCAGAAACATCTCT	674	
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				QY	1102	TCTCCCATGCTGAGCCGCTCAGCGGAAGCGCGACAGAGCGGAAGTCCATGGAAGTCTCTG	1161
REFERENCE	1	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.			Db	975	TCTCCCATGCTGAGCCGCTCAGCGGAAGCGCGACAGAGCGGAAGTCCATGGAAGTCTCTG	1034
AUTHORS	Kits, such as nucleic acid arrays, comprising a majority of				QY	1162	AGCATCACCATGCTCCGGGGTGTGGTCTCCCTGTATCCCAACCGACCGGCTTTGGAGATG	1221
TITLE	humanexons or transcripts, for detecting expression and other uses thereof				Db	1035	AGCATCACCATGCTCCGG-----	1052
JOURNAL	Patent: WO 02068579-A 13184 06-SEP-2002; PE Corporation (NY) (US)				QY	1222	GCCAGCAGACCCAGAGATCCCGTAGGTCAGTGGAGCTCCACGGGTCTGTCTCTCCAGC	1281
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Query Match	45.1%;	Score 1033.2;	DB 6;	Length 1623;	Db	1053	-----	1052
Best Local Similarity	79.6%;	Pred. No. 6.4e-190;			QY	1461	-----	1052
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Gaps	3;				QY	1461	-----	1052
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177	TATTTGACTGTTCTTGGAGCAGCTCTCGGGGGTGTGACTATTGACTACCTGTAAG	236			QY	1461	-----	1052
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Db	1058	-----	1057
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Qy	1588	GGAGCCGCTGGAGGAGTCTCACTCCATCGGCAAGCTTCTGGGCTCCCTCGC	1647
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RESULT 15
AR232171
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DEFINITION Sequence 3 from patent US 6455292.
ACCESSION AR232171
VERSION AR232171.1 GI:27274062
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3364)
AUTHORS Shu, Y., Fan, W., Kovacs, K.F., Zidanic, M. and Jay, G.
TITLE Full-length serine protein kinase in brain and pancreas
JOURNAL Patent: US 6455292-A 3 24-SEP-2002;
FEATURES
1. 3364 Location/Qualifiers
source /organism="unknown"
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ORIGIN

Query Match 34.1%; Score 780.4; DB 6; Length 3364;
Best Local Similarity 68.0%; Pred. No. 5.6e-141;
Matches 1279; Conservative 0; Mismatches 406; Indels 195; Gaps 6;

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Qy	385	GACTTCTGCCACAGCTACTCTCATCTGCCACAGACCTAAAGCCCGAGAAACCTGCTTTTG	444
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Qy	625	CTGCTGGGGCTGCGCCCTTTGATGACGACACACCTCCGCGAGCTGTCGAGAGGTGAAG	684
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Qy	685	CGGGCGCTCTTCCACATGCGCCCTTCACTTCTTCCAGATTGCGAGAGCTCTCTGAGGGGA	744
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Qy	805	TACCTAGGGGGGAAACACGAGCCAGACCCGTCGTCGAGCCAGCCCTGCGCCCGGGTA	864
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Qy 1405 GGTGGGGGCGCGGGGAGACGCCCGCCCCAGTGCOCGCTCCACACCCCTGCCCGGC 1464
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Qy 1465 CCCCCAGGCTCCCGCGCTCTCTGGGGGAGCCCGCTTGCACTCGCTCTGCAACGCCC 1524
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Qy 1525 CGGSCCAGTCCACCGGACCCCGGGACAAACACACCCCGCCAGCCCGGGGTGGGTC 1584
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Qy 1703 CGCTTCCACCGCCGGAACCTCAAGTTCCGACGCCGGAGGAGATGTCCAACTGACACCA 1762
Qy 1705 GAGTCCTCCCGGAGCTGGGAAAACGCTCTCGTTCGGGAACTTCATCTCTCTGGCAAA 1764
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Qy 1823 GAGGAGCAGATCTTCGTGGTTCATCAAGACAAACCTCTGAGTCCATCAAGGCTGACATC 1882
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Qy 1945 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGACGGCAGCGGAGGT 2004
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Job time : 9602 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 08:07:17 ; Search time 1142 Seconds
(without alignments)
11865.401 Million cell updates/sec

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Perfect score: 2289
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2289	100.0	2289	10	ABV74558 Human kin
2	2020.2	88.3	2112	10	ABV74559 Human kin
3	2020.2	88.3	2337	10	ABV74557 Human kin
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5	2020.2	88.3	2385	4	AAS06717 Polynucle
6	2020.2	88.3	2576	10	ADL14127 Novel hum
7	2020.2	88.3	2576	10	ADF74247 Human nov
8	2020.2	88.3	2897	6	AD26464 Human kin
9	2020.2	88.3	2950	13	ADS16433 Human euk
10	2020.2	88.3	2953	9	AAL55772 Human euk
11	2020.2	88.3	2980	10	AD38430 Human pro
12	2020.2	88.3	2980	12	ADL14127 Novel hum
13	2020.2	88.3	2980	13	ADQ85869 Human tum
14	2020.2	88.3	2980	13	ADQ89183 Human uro
15	2020.2	88.3	2980	13	ADS16425 Human euk
16	2017.2	88.1	2334	13	ADS16427 Human euk
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19	980	42.8	1797	8	ABX70994 Novel hum
20	800.8	35.0	1911	9	AAL60438 Human kin

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23	780.4	34.1	3364	12	ADH59077	Adh59077 Human KSE
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28	777.2	34.0	2007	6	ABQ77625	Abq77625 Human kin
29	777.2	34.0	2647	6	AD34315	Ad34315 Human PKI
30	777.2	34.0	3576	13	ADR50785	Adr50785 Human c-b
31	774.8	33.8	2025	9	AAL60436	Aal60436 Human kin
32	774.8	33.8	3831	12	ADJ96555	Adj96555 Human cal
33	773.2	33.8	2025	6	ABA02995	Aba02995 Human pro
34	773.2	33.8	2025	8	ACC48153	Acc48153 Human pro
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37	551	24.1	906	4	ABA08296	Aba08296 Human HrP
38	512	22.4	512	6	ABK70216	Abk70216 Human lun
39	408.4	17.8	584	12	ACH73134	Ach73134 Human gen
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ALIGNMENTS

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AC ABV74558;
XX
DT 20-JAN-2003 (first entry)
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DE Human kinase #2 coding sequence.
XX
KW Human; kinase; chromosome 19; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..2289
FT /*tag= a
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XX
PN WO200281670-A1.
XX
PD 17-OCT-2002.
XX
PP 04-APR-2002; 2002WO-US010786.
XX
PR 06-APR-2001; 2001US-0282036P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Friddle CJ;
XX
DR WPI; 2003-058538/05.
XX
DR P-PSDB; ABB98744.
XX
PT New human kinase proteins useful for diagnosis, drug screening, clinical trial monitoring, treatment of disorders and diseases, and cosmetic and nutritional applications.
XX
PS Claim 5; Page 41-42; 47pp; English.
XX
CC The present sequence is the coding sequence for a novel human kinase. The genomic locus encoding the kinase is thought to be on human chromosome 19. The kinase and its coding sequence are useful for diagnosis, drug

CC	screening, clinical trial monitoring, treatment of disorders and	
CC	diseases, and cosmetic and nutritional applications	
XX		
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	Query Match 100.0%; Score 2289; DB 10; Length 2289;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 2289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Qy	721 GATTCGCGAGCTCTCTGAGGGGAATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTG 780	1681 GAGGAGATGTCCAGCTTGTACGCGCAGAGTCCCTCCCGGAGCTGGCAAAACGCTCTGGTTTC 1740
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Db 2041 GGTCCAGCGCTCGGTTCAAGCGAGTGGTGAGACCATCCAGGCAAGCTCCTGAGCACT 2100
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RESULT 2
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ID ABV74559 standard; cDNA; 2112 BP.
XX AC ABV74559;
XX AC ABV74559;
DT 20-JAN-2003 (first entry)
XX DE Human kinase #3 coding sequence.
XX KW Human; kinase; chromosome 19; gene; ss.
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XX W0200281670-A1.
XX 17-OCT-2002.
XX 04-APR-2002; 2002WO-US010786.
XX 06-APR-2001; 2001US-0282036P.
XX (LEXI-) LEXICON GENETICS INC.
PI Turner CA, Mathur B, Friddle CJ;
XX WPI; 2003-058538/05.
DR P-PSDB; ABB98745.
XX New human kinase proteins useful for diagnosis, drug screening, clinical
PT trial monitoring, treatment of disorders and diseases, and cosmetic and
PT nutritional applications.
XX Claim 5; Page 44; 47pp; English.
XX The present sequence is the coding sequence for a novel human kinase. The
CC genomic locus encoding the kinase is thought to be on human chromosome
CC 19. The kinase and its coding sequence are useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of disorders and
CC diseases, and cosmetic and nutritional applications
XX Sequence 2112 BP; 432 A; 711 C; 615 G; 354 T; 0 U; 0 Other;
SQ

Query Match 88.3%; Score 2020.2; DB 10; Length 2112;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 265 TTTAGGTACTGGTTCTGGAGCACGTCTCGGGGGGTGAGCTATTTCGACTACCTCGTAAAG 324

88 TATTGTACCTGGTTCTGGAGCACGTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 147
325 AAGGGGAGACTGACGCGCCAAAGGAGGCCGAAAGTTCTTCGCGCAGATTTGTGTCTGCCTG 384
148 AAGGGGAGACTGACGCGCCAAAGGAGGCCGAAAGTTCTTCGCGCAGATTTGTGTCTGCCTG 207
385 GACTTCTGCCACAGCTACTCTCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG 444
208 GACTTCTGCCACAGCTACTCTCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG 267
445 GATGAGAAAAAACAATCCGCAATTGCGAGCTTCGCGATGCGCTCCCTGCGAGTGGGGGAC 504
268 GATGAGAAAAAACAATCCGCAATTGCGAGCTTCGCGATGCGCTCCCTGCGAGTGGGGGAC 327
505 AGCCTCCTGAGACCAAGCTGCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTAAAGGG 564
328 AGCCTCCTGAGACCAAGCTGCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTAAAGGG 387
565 GAAAAATATGATGCGCGCGCGGAGACATGTGAGCTGTGAGTGCATCTTTCGCCCTG 624
388 GAAAAATATGATGCGCGCGCGGAGACATGTGAGCTGTGAGTGCATCTTTCGCCCTG 447
625 CTGTTGGGGCTCTGCGCCCTTTGATGACGACAACTCCGCGCAGCTGTGGAGAGAGTCAAA 684
448 CTGTTGGGGCTCTGCGCCCTTTGATGACGACAACTCCGCGCAGCTGTGGAGAGAGTCAAA 507
685 CGGGGGCTCTTCCACATGCCCCCACTTCATCTCTCCAGATTGCCAGAGCCTCTTGAGGGGA 744
508 CGGGGGCTCTTCCACATGCCCCCACTTCATCTCTCCAGATTGCCAGAGCCTCTTGAGGGGA 567
745 ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGAGTCAAAATTCAGAAACATCTTGG 804
568 ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGAGCAAAATTCAGAAACATCTTGG 627
805 TACCTAGCGGGGAAACACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCCCGGGTA 864
628 TACCTAGCGGGGAAACACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCCCGGGTA 687
865 GCCATGCGGAGCCTGCGCATCCAAACGAGAGCTGAGACCCCGACCTCTTAGAGAGCATGGCA 924
688 GCCATGCGGAGCCTGCGCATCCAAACGAGAGCTGAGACCCCGACCTCTTAGAGAGCATGGCA 747
925 TCACTGGGCTGCTTCAGGGACCGCGAGAGCTGATCGCGAGCTGCGCAGTGGAGGAGAG 984
748 TCACTGGGCTGCTTCAGGGACCGCGAGAGCTGATCGCGAGCTGCGCAGTGGAGGAGAG 807
985 AACCAAGAAAGATGATATATTATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGCTGT 1044
808 AACCAAGAAAGATGATATATTATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGCTGT 867
1045 GAGGACCAAGACCTGCGCTCCCGGAAATGATGTTGACCCCCCGGAAACGCTGTGGATTCT 1104
868 GAGGACCAAGACCTGCGCTCCCGGAAATGATGTTGACCCCCCGGAAACGCTGTGGATTCT 927
1105 CCATGCTGAGCCGTCACGCGGAAAGCGCGACACGAGCGGAAGTCCATGGAAGTCTTGAGC 1164
928 CCATGCTGAGCCGTCACGCGGAAAGCGCGACACGAGCGGAAGTCCATGGAAGTCTTGAGC 987
1165 ATCACCGATCGCGGGGTGCTGCTCCCTGTATCCACACCGAGCGGCTTGGAGATGGCC 1224
988 ATCACCGATCGCGGGGTGCTGCTCCCTGTATCCACACCGAGCGGCTTGGAGATGGCC 1047
1225 CAGCAGACCCAGAGATCCCGTAGCGTCAGTGGAGCCCTCCACGGGTCTGTCTCCAGGCCCT 1284
1048 CAGCAGACCCAGAGATCCCGTAGCGTCAGTGGAGCCCTCCACGGGTCTGTCTCCAGGCCCT 1107
1285 CTAAGCAGCCCAAGAGTCCGCTCTTTTCTTTTTCACCGGAGCGGGGTGGAGATGAG 1344
1108 CTAAGCAGCCCAAGAGTCCGCTCTTTTCTTTTTCACCGGAGCGGGGTGGAGATGAG 1167
1345 GCTCGAGCGGGGCTCCCGACTTCCAAAACGAGAGCGTCTTCTCGGGGCCCCCAGG 1404

Db 1168 GCTCAGGCGGGGCTCCCCGACTTCCAAAAACGACAGCTGCTCTCTCGGGGCCCCAGG 1227
XX
Qy 1405 GGTGGGGGCGCGGGAGAGAGCCCCCGCCCCCGAGTCCGCGCTCCACACCCCTGCCCCGGC 1464
Db 1228 GGTGGGGGCGCGGGAGAGAGCCCCCGCCCCCGAGTCCGCGCTCCACACCCCTGCCCCGGC 1287
Qy 1465 CCCCCAGGCTCCCGGGCTCTCTGGCGGAGACCCCTTGCACTCGGCTCTGCACAGCCCC 1524
Db 1288 CCCCCAGGCTCCCGGGCTCTCTGGCGGAGACCCCTTGCACTCGGCTCTGCACAGCCCC 1347
Qy 1525 CGGGCCAGTCCACCGGGACCCCGGGAGAACACACCCCGCCAGCCCCCGGGCGGTGCGTC 1584
Db 1348 CGGGCCAGTCCACCGGGACCCCGGGAGAACACACCCCGCCAGCCCCCGGGCGGTGCGTC 1407
Qy 1585 GGGGAGCCCGCTGGAGGAGTCTCAACTCCATCGGCAACAGCTTCCTGGGCTCCCT 1644
Db 1408 GGGGAGCCCGCTGGAGGAGTCTCAACTCCATCGGCAACAGCTTCCTGGGCTCCCT 1467
Qy 1645 CGCTTTCACCGGCGAAGATGCAGGTCCCTACCGCTGAGGAGATGCCAGCTTGAGGCCA 1704
Db 1468 CGCTTTCACCGGCGAAGATGCAGGTCCCTACCGCTGAGGAGATGCCAGCTTGAGGCCA 1527
Qy 1705 GAGTCTCCCGGAGCTGGCAAAACGCTCTGTTGCGGAACTTCATCTCTTGGACAAA 1764
Db 1528 GAGTCTCCCGGAGCTGGCAAAACGCTCTGTTGCGGAACTTCATCTCTTGGACAAA 1587
Qy 1765 GAAGAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1824
Db 1588 GAAGAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1647
Qy 1825 GTCCATGCTTCTGTGTCATCCCGAGCTGAGTCACAGTGTGTCACAGACAGCTTC 1884
Db 1648 GTCCATGCTTCTGTGTCATCCCGAGCTGAGTCACAGTGTGTCACAGACAGCTTC 1707
Qy 1885 AGGCGGAGTACAGGCGCAGTGGCGGCCCTCTCGTCTTCAAAAGCCGCTCCAG 1944
Db 1708 AGGCGGAGTACAGGCGCAGTGGCGGCCCTCTCGTCTTCAAAAGCCGCTCCAG 1767
Qy 1945 GTGACATCAGCTCTCTGAGGTTCCAGAGCCCTCCCGGACGGGACGGGAGGT 2004
Db 1768 GTGACATCAGCTCTCTGAGGTTCCAGAGCCCTCCCGGACGGGACGGGAGGT 1827
Qy 2005 GGTGGCATCTACTCCGTACCTTCACTCTCATCTCGGGTCCAGCCGTTCAGCGA 2064
Db 1828 GGTGGCATCTACTCCGTACCTTCACTCTCATCTCGGGTCCAGCCGTTCAGCGA 1887
Qy 2065 GTGTGGAGACATCCAGGACAGCTCTGAGCACTCATGACAGCCCTCCGTGACGCC 2124
Db 1888 GTGTGGAGACATCCAGGACAGCTCTGAGCACTCATGAGCACTCATGAGCCCTCCGTGACGCC 1947
Qy 2125 CTGGCAGACGAGAAAGCGGGCCCGACACCCGGGCTGTGTGTGCCCCCAGCCGAGCCTG 2184
Db 1948 CTGGCAGACGAGAAAGCGGGCCCGACACCCGGGCTGTGTGTGCCCCCAGCCGAGCCTG 2007
Qy 2185 CAGCCCCCAGCCGGCCCGCAGACCCAGAGCTGAGAGCTCTCCCGCGAGGCCCCCC 2244
Db 2008 CAGCCCCCAGCCGGCCCGCAGACCCAGAGCTGAGAGCTCTCCCGCGAGGCCCCCC 2067
Qy 2245 AAGGACAAAGAGCTCCTGGCCACCAACCGGACCCCTCTGCCCCGTA 2289
Db 2068 AAGGACAAAGAGCTCCTGGCCACCAACCGGACCCCTCTGCCCCGTA 2112

RESULT 3
ABV74557
ID ABV74557 standard; cDNA; 2337 BP.
XX
AC ABV74557;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human kinase #1 coding sequence.
XX

KW Human; kinase; chromosome 19; gene; ss.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..2337
FT /*tag= a
FT /product= "Human kinase #1"
XX
PN WO200281670-A1.
XX
PD 17-OCT-2002.
XX
PF 04-APR-2002; 2002WO-US010786.
XX
PR 06-APR-2001; 2001US-0282036P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Friddle CJ;
XX
PI WPI; 2003-058538/05.
XX
PI P-PSDB; ABB98743.
XX
PT New human kinase proteins useful for diagnosis, drug screening, clinical
PT trial monitoring, treatment of disorders and diseases, and cosmetic and
PT nutritional applications.
XX
PS Claim 5; Page 39; 47pp; English.
XX
CC The present sequence is the coding sequence for a novel human kinase. The
CC genomic locus encoding the kinase is thought to be on human chromosome
CC 19. The kinase and its coding sequence are useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of disorders and
CC diseases, and cosmetic and nutritional applications
XX
SQ Sequence 2337 BP; 479 A; 786 C; 686 G; 386 T; 0 U; 0 Other;

Query Match 88.3%; Score 2020.2; DB 10; Length 2337;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 265 TTATGATCTACTGTTCTGAGACACGCTCGGGGGTGTGAGTATTGACCTGCTGTAAG 324
Db 313 TATTGTACTGTTCTGAGACACGCTCGGGGGTGTGAGTATTGACCTGCTGTAAG 372
Qy 325 AAGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTCCGCCAGATTGTCTGCGCTG 384
Db 373 AAGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTCCGCCAGATTGTCTGCGCTG 432
Qy 385 GACTTCTGCCACAGTACTTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG 444
Db 433 GACTTCTGCCACAGTACTTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG 492
Qy 445 GATGAGAAAAACAACATCCGATTCGAGACTTTCGGCATGCGCTCCCTGCAGGTGGGGAC 504
Db 493 GATGAGAAAAACAACATCCGATTCGAGACTTTCGGCATGCGCTCCCTGCAGGTGGGGAC 552
Qy 505 AGCCTCTTGAGACAGCTGCGGGTCCCCCATTTATGCTGTCCAGAGTATTAGGGG 564
Db 553 AGCCTCTTGAGACAGCTGCGGGTCCCCCATTTATGCTGTCCAGAGTATTAGGGG 612
Qy 565 GAAAAATATGATGCGCGGCGAGACATGTGAGCTGTGGAGTCACTCTTTCGCGCTG 624
Db 613 GAAAAATATGATGCGCGGCGGAGACATGTGAGCTGTGGAGTCACTCTTTCGCGCTG 672
Qy 625 CTGCTGGGGGCTCTGCGCTTTGATACGACAACTCCGCGAGCTGCTGAGAGAGTGAAG 684
Db 673 CTGCTGGGGGCTCTGCGCTTTGATACGACAACTCCGCGAGCTGCTGAGAGAGTGAAG 732
Qy 685 CGGGCGCTTTCACATGCCCGCTTTCATCTCCAGATTGCGAGAGCTCCTGAGGGGA 744
Db 733 CGGGCGCTTTCACATGCCCGCTTTCATCTCCAGATTGCGAGAGCTCCTGAGGGGA 792

30-SEP-1998; 98US-00163821.
 27-JAN-1999; 99US-0117580P.
 25-MAR-1999; 99US-00276400.
 30-JUL-1998; 99US-00365162.
 09-SEP-1999; 99US-00392189.
 05-OCT-1999; 99US-00412210.
 23-NOV-1999; 99US-00448076.
 29-FEB-2000; 2000US-0186061P.
 28-APR-2000; 2000US-0200688P.
 19-MAY-2000; 2000US-0205447P.
 30-JUN-2000; 2000US-00608921.
 31-JUL-2000; 2000US-0221925P.
 25-SEP-2000; 2000US-0234922P.
 25-SEP-2000; 2000US-0235035P.
 08-NOV-2000; 2000US-0246669P.
 09-NOV-2000; 2000US-00711216.
 14-NOV-2000; 2000US-0248325P.
 15-NOV-2000; 2000US-0248893P.
 22-DEC-2000; 2000US-0257511P.
 05-JAN-2001; 2001US-0260166P.
 28-FEB-2001; 2001US-00797039.
 27-APR-2001; 2001US-00845044.
 20-JUL-2001; 2001US-00909743.
 31-JUL-2001; 2001US-00920346.
 13-AUG-2001; 2001US-00928531.
 14-AUG-2001; 2001US-00929218.
 15-AUG-2001; 2001US-0312539P.
 23-SEP-2001; 2001US-00963159.
 08-NOV-2001; 2001US-00008016.
 13-NOV-2001; 2001US-00012055.
 15-NOV-2001; 2001US-00003690.
 30-JAN-2002; 2002US-00060763.
 25-MAR-2002; 2002US-00105989.
 12-APR-2002; 2002US-00121911.
 12-AUG-2002; 2002US-00217168.
 22-OCT-2002; 2002US-00278036.
 02-JAN-2003; 2003US-00336489.
 03-JAN-2003; 2003US-00336153.
 (MILL-) MILLENNIUM PHARM INC.
 Kapeller-Libermann R, Hunter JJ, Meyers RE, Rudolph-Owen LA;
 Curtis RAJ, Olandt PJ, Tsai F, Galvin KM, Chun M, Williamson MJ;
 Silos-Santiago I, Bandaru R;
 WPI; 2004-268798/25.
 P-PSDB; ADL4128.
 New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529,
 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593
 nucleic acid molecules and proteins, useful for treating, e.g. cancer,
 heart failure and angina.
 Claim 1; SEQ ID NO 12; 139pp; English.
 The invention describes an isolated 21910, 56634, 55053, 2504, 15977,
 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217,
 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising
 any one of 40 nucleotide sequences (I). The nucleic acid molecules and
 polypeptides are useful for diagnosing and treating a subject having a
 disorder, or a subject at risk of developing a disorder, which is
 associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501,
 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983,
 m1983, 38555 or 593 activity, such as cellular proliferative and/or
 differentiative disorders, brain disorders, platelet disorders, breast
 disorders, colon disorders, kidney (renal) disorders, lung disorders,
 ovarian disorders, prostate disorders, cervical disorders, spleen
 disorders, thymus disorders, thyroid disorders, testes disorders,
 hematopoietic disorders, pancreatic disorders, skeletal muscle disorders,
 skin (dermal) disorders, disorders associated with bone metabolism,
 immune, e.g. inflammatory disorders, cardiovascular disorders,
 endothelial cell disorders, liver disorders, viral diseases, pain
 disorders, metabolic disorders, neurological or central nervous system

Db 361 TATTTGTACCTGTTCTGAGCAGCTCTCGGGGGTGAGCTATTGACTACCTGTGTAAG 420
Qy 325 AAGGGAGACTGACGGCCCAAGAGGCCCGAAGTTCTTCGGCAGATTGTGTCTGCGTG 384
Db 421 AAGGGAGACTGACGGCCCAAGAGGCCCGAAGTTCTTCGGCAGATTGTGTCTGCGTG 480
Qy 385 GACTTCTGCGCACAGCTACTCTCATCTGCCACAGAGACTTAAAGCCCGAGAACCTGCTTTTG 444
Db 481 GACTTCTGCGCACAGCTACTCTCATCTGCCACAGAGACTTAAAGCCCGAGAACCTGCTTTTG 540
Qy 445 GATGAGAAAAACAATCCGCATTGCGCATTCGCGATGCGGTCCTGCGAGGTGGGGAC 504
Db 541 GATGAGAAAAACAATCCGCATTGCGCATTCGCGATGCGGTCCTGCGAGGTGGGGAC 600
Qy 505 AGCTCTGAGACCAAGCTCGGGTCCCGCATTTATGCGTGTCCAGAGGTGATTAAGGG 564
Db 601 AGCTCTGAGACCAAGCTCGGGTCCCGCATTTATGCGTGTCCAGAGGTGATTAAGGG 660
Qy 565 GAAAAATATGATGGCCCGCGGCGAGACATGTGAGCTGTGGAGTCAATCTTTCGCCCTG 624
Db 661 GAAAAATATGATGGCCCGCGGCGAGACATGTGAGCTGTGGAGTCAATCTTTCGCCCTG 720
Qy 625 CTGCTGGGGGCTTGCCCTTTGATGACGACAACTCGGCCAGCTGTGGAGAGGTGAAA 684
Db 721 CTGCTGGGGGCTTGCCCTTTGATGACGACAACTCGGCCAGCTGTGGAGAGGTGAAA 780
Qy 685 CGGGGCTCTTCCACATGCCCTTCAATCTCCAGATTGCCAGAGCTCTCTGAGGGGA 744
Db 781 CGGGGCTCTTCCACATGCCCTTCAATCTCTCCAGATTGCCAGAGCTCTCTGAGGGGA 840
Qy 745 ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAATCTCTTG 804
Db 841 ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAATCTCTTG 900
Qy 805 TACTAGCGGGAACAGAGCCAGACCGTGTCTGGAGCCAGCCCTGCGCCCGGGTA 864
Db 901 TACTAGCGGGAACAGAGCCAGACCGTGTCTGGAGCCAGCCCTGCGCCCGGGTA 960
Qy 865 GCCATGCGGAGCTGCCATCCAAACGAGAGCTGACGCCCGCCAGCTCTTAGAGAGCATGGCA 924
Db 961 GCCATGCGGAGCTGCCATCCAAACGAGAGCTGACGCCCGCCAGCTCTTAGAGAGCATGGCA 1020
Qy 925 TCATGCGGCTCTTCAGGGAACCGAGAGGTGATCGGAGCTGCCAGTGGAGGAG 984
Db 1021 TCATGCGGCTCTTCAGGGAACCGAGAGGTGATCGGAGCTGCCAGTGGAGGAG 1080
Qy 985 AACCAAGAAAGATGATATATTATCTGTTTGGATCGAAGAGCGGTATCCAGCTGT 1044
Db 1081 AACCAAGAAAGATGATATATTATCTGTTTGGATCGAAGAGCGGTATCCAGCTGT 1140
Qy 1045 GAGGACCAAGGACCTGCTCTCCCGGAATGATTTGACCCCGGAAAGCGGTGATCT 1104
Db 1141 GAGGACCAAGGACCTGCTCTCCCGGAATGATTTGACCCCGGAAAGCGGTGATCT 1200
Qy 1105 CCATGCTGAGCCGTACGGGAAGCGGACAGAGCGGAGTCCATGGAAGTCTTGAGC 1164
Db 1201 CCATGCTGAGCCGTACGGGAAGCGGACAGAGCGGAGTCCATGGAAGTCTTGAGC 1260
Qy 1165 ATCCCGATGCGGGGTGGTGGCTCCCTGTACCCACCGAGCGGCTTGAGATGGCC 1224
Db 1261 ATCCCGATGCGGGGTGGTGGCTCCCTGTACCCACCGAGCGGCTTGAGATGGCC 1320
Qy 1225 CAGCACAGCAGAGATCCCGTATGAGTGTGAGAGCTCAGGGTCTGTCTCCAGCCCT 1284
Db 1321 CAGCACAGCAGAGATCCCGTATGAGTGTGAGAGCTCAGGGTCTGTCTCCAGCCCT 1380
Qy 1285 CTAAGCAGCCCAAGAGTCCGCTTTCTTTCACCGGAGCCGGGGCTTGAGATGAG 1344
Db 1381 CTAAGCAGCCCAAGAGTCCGCTTTCTTTCACCGGAGCCGGGGCTTGAGATGAG 1440
Qy 1345 GCTCAGAGCGGGGCTCCCGCACTTCCAAAACGACAGAGCTGCTTCTCGGGGCCAGG 1404
Db 1441 GCTCAGAGCGGGGCTCCCGCACTTCCAAAACGACAGAGCTGCTTCTCGGGGCCAGG 1500

Qy 1405 GGTGGGGGCGCGGGGAGCAGCCCCCGCCAGTGGCCCGCTCCACACCCCTGCCCCGC 1464
Db 1501 GGTGGGGGCGCGGGGAGCAGCCCCCGCCAGTGGCCCGCTCCACACCCCTGCCCCGC 1560
Qy 1465 CCCCAGAGCTCCCGCGCTCTCTGGGGGAGCCCTTGGCACTGCTCTGCAACAGGCC 1524
Db 1561 CCCCAGAGCTCCCGCGCTCTCTGGGGGAGCCCTTGGCACTGCTCTGCAACAGGCC 1620
Qy 1525 CGGGCAGTCCACACCGGACCCCGGGGACAAACACACCCCGAGCCCGGGTGGCGTC 1584
Db 1621 CGGGCAGTCCACACCGGACCCCGGGGACAAACACACCCCGAGCCCGGGTGGCGTC 1680
Qy 1585 GGGGAGCGCTGAGAGTGTCTCAACTCCATCCGCAACAGTCTCTGGCTCCCT 1644
Db 1681 GGGGAGCGCTGAGAGTGTCTCAACTCCATCCGCAACAGTCTCTGGCTCCCT 1740
Qy 1645 CGCTTTCACCGGCGCAAGATGAGGTCCCTACCGCTGAGGAGATGTCAGCTTGAAGCA 1704
Db 1741 CGCTTTCACCGGCGCAAGATGAGGTCCCTACCGCTGAGGAGATGTCAGCTTGAAGCA 1800
Qy 1705 GAGTCTCCCGGAGCTGGCAAAACGCTCTGCTGGTTGGGAACTTCACTCTCTTGAACAA 1764
Db 1801 GAGTCTCCCGGAGCTGGCAAAACGCTCTGCTGGTTGGGAACTTCACTCTCTTGAACAA 1860
Qy 1765 GAAGAACAAATATTCTGTGCTTAAAGACAAACCTCTCAGCAGCATCAAAGCAGCATC 1824
Db 1861 GAAGAACAAATATTCTGTGCTTAAAGACAAACCTCTCAGCAGCATCAAAGCAGCATC 1920
Qy 1825 GTCCATGCTTCTGTGATCCCGAGCTGAGTCAAGTGTCTGTCTCAGACCCAGCTTC 1884
Db 1921 GTCCATGCTTCTGTGATCCCGAGCTGAGTCAAGTGTCTGTCTCAGACCCAGCTTC 1980
Qy 1885 AGGGCCGAGTCAAGGCGAGTGGCGGCCCTCCGCTCTTCCAAAAGCCGCTCCGCTTCAG 1944
Db 1981 AGGGCCGAGTCAAGGCGAGTGGCGGCCCTCCGCTCTTCCAAAAGCCGCTCCGCTTCAG 2040
Qy 1945 GTGGACATCAGCTCTCTGAGGCTCCAGAGCTCCCGCGACGGGACGGCAGCGAGGT 2004
Db 2041 GTGGACATCAGCTCTCTGAGGCTCCAGAGCTCCCGCGACGGGACGGCAGCGAGGT 2100
Qy 2005 GGTGGCATCTACTCCGTCACTCTCACTCTCGGTCCAGCCGTCGCTTCAAGCA 2064
Db 2101 GGTGGCATCTACTCCGTCACTCTCACTCTCGGTCCAGCCGTCGCTTCAAGCA 2160
Qy 2065 GTGGTGGACCATCCAGCAGCTCTGAGCAGCTCATGACAGCCCTCCGCTGAGGCT 2124
Db 2161 GTGGTGGACCATCCAGCAGCTCTGAGCAGCTCATGACAGCCCTCCGCTGAGGCT 2220
Qy 2125 CTGGCAGACGAGAAACCGGGGCCAGAGCCCGGCTGTGGTGGCCCGACCCGAGCCCTG 2184
Db 2221 CTGGCAGACGAGAAACCGGGGCCAGAGCCCGGCTGTGGTGGCCCGACCCGAGCCCTG 2280
Qy 2185 CAGCCCCCAGCCCGGCCCGCAGACCCAGAGCTGAGAGCTCTCCCGCGAGGCCCCCCC 2244
Db 2281 CAGCCCCCAGCCCGGCCCGCAGACCCAGAGCTGAGAGCTCTCCCGCGAGGCCCCCCC 2340
Qy 2245 AAGGACNAGAGCTCTTGGCCACCAAGCGGAGCCCTCTGCGCTGA 2289
Db 2341 AAGGACNAGAGCTCTTGGCCACCAAGCGGAGCCCTCTGCGCTGA 2385

RESULT 6

ADE71237
ID ADE71237 standard; DNA; 2576 BP.

XX ADE71237;

XX AC AC

XX XX XX

XX 29-JAN-2004 (first entry)

XX Novel human protein coding sequence #53.

XX human; novel protein; drug; gene; ds.

KW

QY 2005 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGTTCCACGCGTGGTTCAAGCGA 2064
DB 1865 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGTTCCACGCGTGGTTCAAGCGA 1924
QY 2065 GTGGTGAGACCATCCAGGACACAGCTCTCTGAGCACTCATGACAGCCCTCCGTCGAGGCC 2124
DB 1925 GTGGTGAGACCATCCAGGACACAGCTCTCTGAGCACTCATGACAGCCCTCCGTCGAGGCC 1984
QY 2125 CTGGCAGACGAGAAAGCGGGGCCAGACCCGGCGCTGCTGGTCCGCCACCCCGAAGCCTG 2184
DB 1985 CTGGCAGACGAGAAAGCGGGGCCAGACCCGGCGCTGCTGGTCCGCCACCCCGAAGCCTG 2044
QY 2185 CAGCCCCACCGCGCCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGGAGGCCCCCC 2244
DB 2045 CAGCCCCACCGCGCCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGGAGGCCCCCC 2104
QY 2245 AAGGACAAAGAGTCTCTGGCCACCAACGCGGACCCCTCTGCCCTGA 2289
DB 2105 AAGGACAAAGAGTCTCTGGCCACCAACGCGGACCCCTCTGCCCTGA 2149

RESULT 7

ADF74247
ID ADF74247 standard; cDNA; 2576 BP.

AC ADF74247;

XX 26-FEB-2004 (first entry)

XX Human novel brain/hippocampus cDNA #65.

XX Human; brain; hippocampus; gene therapy; mental illness;

XX proteome analysis; ss; Gene.

XX Homo sapiens.

XX JP2003009886-A.

XX 14-JAN-2003.

XX 21-DEC-2001; 2001JP-00390441.

XX 22-DEC-2000; 2000JP-00389742.

XX 29-MAR-2001; 2001JP-00095524.

XX 25-APR-2001; 2001JP-00127066.

XX (KAZU-) ZH KAZUSA DNA KENKYUSHO.

XX (PROT-) PROTEIN EXPRESS KK.

XX WPI; 2003-735084/70.

XX P-PSDB; ADF74177.

XX Novel isolated polypeptide useful for screening compounds which modulate the activity of polypeptide and thus have therapeutic applications.

XX Disclosure; SEQ ID NO 135; 319pp; Japanese.

XX The invention relates to an isolated human polypeptide consisting of a sequence of any one of 70 fully defined sequences (S1) appearing as ADF74113-ADF74182 being encoded by one of 70 disclosed cDNA sequences isolated from brain or hippocampus tissue, or a sequence of (S1) having deletion, substitution, or addition and essentially retaining the same biological activity of (S1). Also included are DNA that encodes the protein, DNA which hybridizes with the encoding DNA and codes a polypeptide which substantially as the same activity as that of a polypeptide above, a gene including the DNA, a recombinant polypeptide encoded by the gene, an antibody against the protein, DNA chip which comprises the DNA, a polypeptide chip comprising the protein, an antibody comprising the antibody, a recombinant vector containing the DNA, a transformed host cell containing the vector, an antisense polynucleotide which has a sequence complementary to the DNA, a kit for screening compounds that interact with the protein, test compounds which interact

CC with the protein and homologous proteins having 70% sequence identity CC with (S1). The protein is useful for identifying compounds which interact CC with the protein e.g., compounds which inhibit or activate the protein. CC Compounds that inhibit the protein activity are useful as therapeutic CC agents for treating disorders characterized by aberrant protein activity. CC The DNA is useful for producing the protein by recombinant techniques, as CC a probe in diagnostic techniques for detecting abnormalities in the gene, CC and in gene therapy techniques. The DNA is useful for creating animal CC models of disease. The DNA chips are useful for diagnosing any CC abnormalities of the DNA in biological samples obtained from human CC subjects, where the abnormalities result in mental illness. The antibody CC is useful for detecting the protein in biological samples. The protein CC chip is useful for functional analysis of the protein, e.g. expression of CC the protein, interaction of the protein, post-translational modification CC of the protein. The antibody chip is useful for analysing disease states CC associated with polypeptide. The antibody chip is also useful in proteome CC analysis. The present sequence encodes a human brain/hippocampus protein CC of the invention.

XX Sequence 2576 BP; 508 A; 842 C; 766 G; 460 T; 0 U; 0 Other;

QY Query Match 88.3%; Score 2020.2; DB 10; Length 2576;

DB Best Local Similarity 99.9%; Pred. No. 0;

XX Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 265 TTTAGGTACTCGTTCCTGGAGCACGTTCTCGGGGGTGTGAGCTATTGACTTACCTGTAAG 324

DB 125 TATTTGTACTCGTTCCTGGAGCACGTTCTCGGGGGTGTGAGCTATTGACTTACCTGTAAG 184

QY 325 AAGGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTCCGCCAGATTCTGTCTGCGCTG 384

DB 185 AAGGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTCCGCCAGATTCTGTCTGCGCTG 244

QY 385 GACTTCTGCCACAGCTACTCTCATCTGCCACAGAGACCTAAAGCCGAGAACCTGCTTTTG 444

DB 245 GACTTCTGCCACAGCTACTCTCATCTGCCACAGAGACCTAAAGCCGAGAACCTGCTTTTG 304

QY 445 GATGAGAAAAACATCCGCAITGAGACTTCCGATCGGCTCCGCTCCAGGTGGGGGAC 504

DB 305 GATGAGAAAAACATCCGCAITGAGACTTCCGATCGGCTCCGCTCCAGGTGGGGGAC 364

QY 505 AGCTCTCTGGAGACAGCTCGGGTCCGCCCATTTATGCGTGTCCAGAGGTGATTAAGGGG 564

DB 365 AGCTCTCTGGAGACAGCTCGGGTCCGCCCATTTATGCGTGTCCAGAGGTGATTAAGGGG 424

QY 565 GAAAAATATGATGGCCGCCGCGGACATGTGAGCTGTGAGTCACTCTTCGCGCTG 624

DB 425 GAAAAATATGATGGCCGCCGCGGACATGTGAGCTGTGAGTCACTCTTCGCGCTG 484

QY 625 CTGCTGGGGCTCTGCCCTTTGATGACGACACCTCCGCCAGCTGCGAGAGGTGAA 684

DB 485 CTGCTGGGGCTCTGCCCTTTGATGACGACACCTCCGCCAGCTGCGAGAGGTGAA 544

QY 685 CGGGGGCTCTTCCACATGCCCCACTTTCATTCCTCCAGATTGCCAGAGCTCTTCGAGGGGA 744

DB 545 CGGGGGCTCTTCCACATGCCCCACTTTCATTCCTCCAGATTGCCAGAGCTCTTCGAGGGGA 604

QY 745 ATGATCGAAGTGGAGCCCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG 804

DB 605 ATGATCGAAGTGGAGCCCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG 664

QY 805 TACTTAGCGGGGAAACACGAGCCGAGACCCGCTGCTGAGCCAGCCCTCGCCCGCGGTA 864

DB 665 TACTTAGCGGGGAAACACGAGCCGAGACCCGCTGCTGAGCCAGCCCTCGCCCGCGGTA 724

QY 865 GGCATCGGAGCTGCTGCATCCAAACGGAGAGCTGGACCCCGACCTCTCTAGAGAGATGGCA 924

DB 725 GGCATCGGAGCTGCTGCATCCAAACGGAGAGCTGGACCCCGACCTCTCTAGAGAGATGGCA 784

QY 925 TCATCGGGCTGCTTCAGGACCCGAGAGAGCTGCATCGGAGCTGCGCAGCTGGAGGAG 984

DB 785 TCATCGGGCTGCTTCAGGACCCGAGAGAGCTGCATCGGAGCTGCGCAGCTGGAGGAG 844

985 AACCAAGAAAGATGATATATTATCTGCTTTTGGATCGAAGGAGCGGTATCCAGCTGT 1044
845 AACCAAGAAAGATGATATATTATCTGCTTTTGGATCGAAGGAGCGGTATCCAGCTGT 904
1045 GAGGACCAAGGACCTGCTCCCGGAATGATGTTGACCCCGCCCGGAAGCGTGTGGATTCT 1104
905 GAGGACCAAGGACCTGCTCCCGGAATGATGTTGACCCCGCCCGGAAGCGTGTGGATTCT 964
1105 CCATGCTGAGCCCTCAAGGAGCGGCGGACGAGCGGAGTTCATGGAAGTCTCTGAGC 1164
965 CCATGCTGAGCCCTCAAGGAGCGGCGGACGAGCGGAGTTCATGGAAGTCTCTGAGC 1024
1165 ATACCCGATGCGGGGGTGTGGCTCCCTGCTACCCACCGAGCGGGCTTGGAGATGGCC 1224
1025 ATACCCGATGCGGGGGTGTGGCTCCCTGCTACCCACCGAGCGGGCTTGGAGATGGCC 1084
1225 CAGCACGACGAGATCCCGTAGCGTCAGTGGAGCTCCACGGGTCTGTCTCCAGCCCT 1284
1085 CAGCACGACGAGATCCCGTAGCGTCAGTGGAGCTCCACGGGTCTGTCTCCAGCCCT 1144
1285 CTAAAGACCCCAAGGATGCTGCTTTTCTTTTCAACGAGCGCGGGCTGGAGATGAG 1344
1145 CTAAAGACCCCAAGGATGCTGCTTTTCTTTTCAACGAGCGCGGGCTGGAGATGAG 1204
1345 GCTCGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTCGGGGCCCCCAGG 1404
1205 GCTCGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTCGGGGCCCCCAGG 1264
1405 GGTGGGGGCGCGGGGAGCAGCCCCCGCCCGAGTCCCGCTCCACACCCCTGCCCCGGC 1464
1265 GGTGGGGGCGCGGGGAGCAGCCCCCGCCCGAGTCCCGCTCCACACCCCTGCCCCGGC 1324
1465 CCCCCAGGCTCCCGCGCTCTCTGCGGGGACCCCCCTTGCACTGCTCTGCAACGCC 1524
1325 CCCCCAGGCTCCCGCGCTCTCTGCGGGGACCCCCCTTGCACTGCTCTGCAACGCC 1384
1525 CGGGCAGTCCACCGGAGCCCCGGGAGCAACACACCCCGCCAGCCCCGGGGTGGCGTC 1584
1385 CGGGCAGTCCACCGGAGCCCCGGGAGCAACACACCCCGCCAGCCCCGGGGTGGCGTC 1444
1585 GGGGAGCGCGCTGGAGAGTGGTCTCAATCCATCCGCAACAGCTTCTCGGGCTCCCT 1644
1445 GGGGAGCGCGCTGGAGAGTGGTCTCAATCCATCCGCAACAGCTTCTCGGGCTCCCT 1504
1645 CGCTTTCAACCGGCAAGATGAGTCCCTACCGCTGAGGAGATGTCAGCTTTGACGCCA 1704
1505 CGCTTTCAACCGGCAAGATGAGTCCCTACCGCTGAGGAGATGTCAGCTTTGACGCCA 1564
1705 GAGTCTCTCCCGGAGCTGGGCAAAACGCTCTGTTTGGGAACTTCATCTCTTGGAGAA 1764
1565 GAGTCTCTCCCGGAGCTGGGCAAAACGCTCTGTTTGGGAACTTCATCTCTTGGAGAA 1624
1765 GAAGAACAAATATCTCGTGTAAAGAGCAAAACCTCTCAGCAGCATCAAGCAGCATC 1824
1625 GAAGAACAAATATCTCGTGTAAAGAGCAAAACCTCTCAGCAGCATCAAGCAGCATC 1684
1825 GTCCATGCTTTCTGTGATGCCCGGAGCTGAGTCCAGTGTGCTGTGTCACAGCAGCTTC 1884
1685 GTCCATGCTTTCTGTGATGCCCGGAGCTGAGTCCAGTGTGCTGTGTCACAGCAGCTTC 1744
1885 AGGGCCGAGTACAAGGCGAGTGGGGCCCTTCGCTTCCAAAGCCCGTCCGTTCCAG 1944
1745 AGGGCCGAGTACAAGGCGAGTGGGGCCCTTCGCTTCCAAAGCCCGTCCGTTCCAG 1804
1945 GTGACATCAGCTCTCTGAGGTCAGAGCCCTCCCGGAGCGGAGCGGAGGAGGT 2004
1805 GTGACATCAGCTCTCTGAGGTCAGAGCCCTCCCGGAGCGGAGCGGAGGAGGT 1864
2005 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGGTTCAAGCGA 2064
1865 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGGTTCAAGCGA 1924
2065 GTGGTGGAGACCATCCAGGCGACAGCTCTCTGAGCACTCATGACCGCCCTCCGTGCAGGCC 2124

1925 GTGGTGGAGACCATCCAGGCAAGCTCTCTGAGCACTCATGACCAAGCCCTCCGTGCAGGCC 1984
2125 CTGGCAGACGAGAAAGAACCGGGCCCGAGACCCGGCCTCTGCTGGTCCCGACCCCGAAGCCTG 2184
1985 CTGGCAGACGAGAAAGAACCGGGCCCGAGACCCGGCCTCTGCTGGTCCCGACCCCGAAGCCTG 2044
2185 CAGCCCGCCCGCCCGCCCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCCCCC 2244
2045 CAGCCCGCCCGCCCGCCCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCCCCC 2104
2245 AAGGACAAAGAGCTCTCTGGCCACCAACGAGGACCCCTCTGCCCCTGA 2289
2105 AAGGACAAAGAGCTCTCTGGCCACCAACGAGGACCCCTCTGCCCCTGA 2149

RESULT 8
AAD26464
ID AAD26464 standard; cDNA; 2897 BP.
XX AAD26464;
AC AAD26464;
XX
DT 26-MAR-2002 (first entry)
XX
XX Human kinase PKIN-17 cDNA.
DE
XX
XX Human; kinase; PKIN-17; cancer; leukaemia; adenocarcinoma; osteoporosis;
KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW fatty liver; Niemann-Pick's disease; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
CDS 1..2385
FT /*tag= a /product= "Human PKIN-17 protein"
FT
XX
XX WO200196547-A2.
XX
XX
PD 20-DEC-2001.
XX
XX 14-JUN-2001; 2001WO-US019444.
XX
XX 15-JUN-2000; 2000US-0212073P.
PR 23-JUN-2000; 2000US-0213467P.
PR 30-JUN-2000; 2000US-0215651P.
PR 07-JUL-2000; 2000US-0216605P.
PR 13-JUL-2000; 2000US-0218372P.
PR 25-AUG-2000; 2000US-0228056P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
PI Gandhi AR, Tribouley CM, Wallia NK, Yao MG, Lu DAM, Greenwald SR;
PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YF;
PI Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
XX
XX WPI; 2002-090207/12.
DR P-PSDB; AAE16271.
XX
XX New polypeptides, useful for diagnosing, treating or preventing disorders
PT of growth and development, cardiovascular and lipid, and diseases such as
PT cancer, comprise human kinase polypeptides.

Db 2041 GTGACATCAGCTCTCTGAGGTCAGAGCCCTCCCGCGACCGGACGGCGGAGGT 2100
Qy 2005 GGTGGCATCTACTCGTCCACTTCACTCTCACTCTCGGTCCTCCAGCCGTCGGTTCAAGCGA 2064
Db 2101 GGTGGCATCTACTCGTCCACTTCACTCTCACTCTCGGTCCTCCAGCCGTCGGTTCAAGCGA 2160
Qy 2065 GTGCTGAGACATCCAGGACAGCTCTGAGCACTATGACAGCCCTCGTGCAGGCC 2124
Db 2161 GTGCTGAGACATCCAGGACAGCTCTGAGCACTATGACAGCCCTCGTGCAGGCC 2220
Qy 2125 CTGCGACAGCAGAGAACGGGCGCCAGACCCGGCTCTGTGTGTCGCCACCCCGAAGCCTG 2184
Db 2221 CTGCGAGCAGAGAACGGGCGCCAGACCCGGCTCTGTGTGTCGCCACCCCGAAGCCTG 2280
Qy 2185 CAGCCCCACCGCGCCGCGCCAGACCCAGCTGAGCAGCTCTCCCGCCGAGGCCCCCCCC 2244
Db 2281 CAGCCCCACCGCGCCGCGCCAGACCCAGCTGAGCAGCTCTCCCGCCGAGGCCCCCCCC 2340
Qy 2245 AAGCACAAGAAGCTCTGCGCCACCAACCGGACCCCTCTGCCCTGA 2289
Db 2341 AAGCACAAGAAGCTCTGCGCCACCAACCGGACCCCTCTGCCCTGA 2385

RESULT 9
ADS16433
ID ADS16433 standard; cDNA; 2950 BP.
AC ADS16433;
XX
XX 18-NOV-2004 (first entry)
XX Human eukaryotic protein kinase-55053 (EPK-55053) cDNA #2.
KW Eukaryotic protein kinase-55053; EPK-55053; CNS disorder;
KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;
KW amyotrophic lateral sclerosis; epilepsy; autonomic function disorder;
KW sleep disorder; depression; mania; anxiety disorder; phobic disorder;
KW learning disorder; memory disorder; amnesia; attention deficit disorder;
KW cardiovascular system disorder; arteriosclerosis; ischaemia;
KW reperfusion injury; restenosis; vascular heart disease;
KW hormonal disorder; diabetes; thyroid disorder; reproductive disorder;
KW fertility disorder; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; hypnotic; antidepressant; antimanic; tranquiliser;
KW cardiovascular; antiarteriosclerotic; vasotropic; antidiabetic;
KW antithyroid; gynaecological; human; gene; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 86..2422
FT /*tag= a
FT /product= "Eukaryotic protein kinase-55053 (EPK-55053)"
XX
XX US6787345-B1.
XX
XX 07-SEP-2004.
XX
XX 15-NOV-2001; 2001US-00003690.
XX
XX 15-NOV-2000; 2000US-0248893P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Curtis RAJ;
XX
XX WPI; 2004-632931/61.
DR P-PSDB; ADS16426.
XX
XX New isolated eukaryotic kinase (EPK-55053) nucleic acid and protein,
XX useful for diagnosing or treating EPK-55053 mediated or related
XX disorders, e.g. Alzheimer's disease, multiple sclerosis, depression,
XX ischemia, restenosis, or diabetes.

XX Example 1; Fig 1; 55pp; English.
XX
CC The invention relates to an eukaryotic protein kinase-55053 (EPK-55053)
CC and its corresponding nucleic acid sequence. The EPK-55053 nucleic acid
CC molecules, proteins and antibodies are useful in screening assays,
CC diagnostic assays, prognostic assays, in monitoring clinical trials,
CC pharmacogenetics or for treating EPK-55053 mediated or related disorders.
CC EPK-55053 mediated or related disorders include CNS disorders
CC (Alzheimer's disease, Parkinson's disease, multiple sclerosis,
CC amyotrophic lateral sclerosis or epilepsy), autonomic function disorders
CC (sleep disorders, depression, mania, anxiety disorders or phobic
CC disorders), learning or memory disorders (amnesia or attention deficit
CC disorder), cardiovascular system disorders (arteriosclerosis, ischaemia,
CC reperfusion injury, restenosis or vascular heart disease), hormonal
CC disorders (diabetes or thyroid disorders) and reproductive or fertility
CC disorders. The present sequence is human EPK-55053 cDNA. Note: This
CC sequence is stated to be similar to the sequence shown as SEQ ID NO:1 in
CC the sequence listing of the specification. However this does not appear
CC to be the case.
XX
XX Sequence 2950 BP; 606 A; 955 C; 880 G; 509 T; 0 U; 0 Other;
SQ
Query Match 88.3%; Score 2020.2; DB 13; Length 2950;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 265 TTTAGGTACCTGGTTCTGGAGCAGCTCTCGGGGGGTGAGCTATTGCACTACCTGGTAAAG 324
Db 398 TATTGTACCTGGTTCTGGAGCAGCTCTCGGGGGGTGAGCTATTGCACTACCTGGTAAAG 457
Qy 325 AAGGGAGACTGACGCCAAGGAGGCCGAAAGTTCTTCGCCAGATGTGTTCGCCGTG 384
Db 458 AAGGGAGACTGACGCCAAGGAGGCCGAAAGTTCTTCGCCAGATGTGTTCGCCGTG 517
Qy 385 GACTTCTGCCACAGCTACTCCATCTGCGACAGACCTTAAGCCCGAGAGACCTGCTTTTG 444
Db 518 GACTTCTGCCACAGCTACTCCATCTGCGACAGACCTTAAGCCCGAGAGACCTGCTTTTG 577
Qy 445 GATGAGAAAAACAACATCCCATTCGACAGCTTCGGCATGGCTCCCTCGAGGTGGGGAC 504
Db 578 GATGAGAAAAACAACATCCCATTCGACAGCTTCGGCATGGCTCCCTCGAGGTGGGGAC 637
Qy 505 AGCCTCTCGAGACAGCTCGGGTCCGCCATATGCGTGTCCAGAGGTGATTAAGGG 564
Db 638 AGCCTCTCGAGACAGCTCGGGTCCGCCATATGCGTGTCCAGAGGTGATTAAGGG 697
Qy 565 GAAAAATATGATGGCCCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTCGCCCTG 624
Db 698 GAAAAATATGATGGCCCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTCGCCCTG 757
Qy 625 CTGCTGGGGGCTCTGCCCTTTTGATGACGACAACTCCCGCAGCTGTGGAGAGGTGAAA 684
Db 758 CTGCTGGGGGCTCTGCCCTTTTGATGACGACAACTCCCGCAGCTGTGGAGAGGTGAAA 817
Qy 685 CGGGGGGTCTTCCACATGCCCACTTCAATTCCTCCAGATTGCCAGAGCCTCTTGAGGGGA 744
Db 818 CGGGGGGTCTTCCACATGCCCACTTCAATTCCTCCAGATTGCCAGAGCCTCTTGAGGGGA 877
Qy 745 ATGATCGAAGTGGAGCCCGGAAAAAGGCTCAGTCTGGAGCAATTCAGAAACATCTTGG 804
Db 878 ATGATCGAAGTGGAGCCCGGAAAAAGGCTCAGTCTGGAGCAATTCAGAAACATCTTGG 937
Qy 805 TACTTAGCGGGGAAACACGAGCCAGACCCGTGTCTGGAGCCAGCCCTCGGCCCGGGTA 864
Db 938 TACTTAGCGGGGAAACACGAGCCAGACCCGTGTCTGGAGCCAGCCCTCGGCCCGGGTA 997
Qy 865 GCCATCGGAGCCTGCGCATCCAAACGAGAGCTGAGACCCCGACGCTCTTAGAGAGCATGCCA 924
Db 998 GCCATCGGAGCCTGCGCATCCAAACGAGAGCTGAGACCCCGACGCTCTTAGAGAGCATGCCA 1057
Qy 925 TCACTGGGCTGTCTTAGGAGACCGGAGAGGCTGATCGCGAGCTGCCAGTGGCAGTAGGAGAG 984

Db 1058 TCACTGGGCTGCTTCAGGACCCGAGAGAGGCTGCATCGCGAGTGCAGTGAGGAGAG 1117
Qy 985 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1044
Db 1118 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1177
Qy 1045 GAGGACCAAGACTGCTCCCGGGAATGATGTTGACCCCGGGAAGCGTGTGGATTCT 1104
Db 1178 GAGGACCAAGACTGCTCCCGGGAATGATGTTGACCCCGGGAAGCGTGTGGATTCT 1237
Qy 1105 CCCATGTGAGCCGTTCACGGGAAGCGGCGACGAGCGGAAGTCCATGGAAGTCTTGAGC 1164
Db 1238 CCCATGTGAGCCGTTCACGGGAAGCGGCGACGAGCGGAAGTCCATGGAAGTCTTGAGC 1297
Qy 1165 ATCAACGATGCGGGGTGTGGTCCCTGTCACCCGACCGAGCGGCTTGGAGTGGCC 1224
Db 1298 ATCAACGATGCGGGGTGTGGTCCCTGTCACCCGACCGAGCGGCTTGGAGTGGCC 1357
Qy 1225 CAGCACAGCCAGATCCCGTAGGCTCAGTGGAGCTTCCACGGGTCTGTCTCCAGCCCT 1284
Db 1358 CAGCACAGCCAGATCCCGTAGGCTCAGTGGAGCTTCCACGGGTCTGTCTCCAGCCCT 1417
Qy 1285 CTAAAGCAGCCCAAGAGTCCGGTCTTTTCCATCCAGGAGCGGGGCTGGAGATGAG 1344
Db 1418 CTAAAGCAGCCCAAGAGTCCGGTCTTTTCCATCCAGGAGCGGGGCTGGAGATGAG 1477
Qy 1345 GCTGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTTCGCGGCCCCAGG 1404
Db 1478 GCTGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTTCGCGGCCCCAGG 1537
Qy 1405 GGTGGGCGCGGGGAGCAGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCGG 1464
Db 1538 GGTGGGCGCGGGGAGCAGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCGG 1597
Qy 1465 CCCCAGGCTCCCGCGTCTCTGCGGGAGACCCCTTGCATCGCTCTGCAACGCC 1524
Db 1598 CCCCAGGCTCCCGCGTCTCTGCGGGAGACCCCTTGCATCGCTCTGCAACGCC 1657
Qy 1525 CGGGCAGTCCACCGGACCCCGGGGACACACACCCCGCCAGCCCGGGGTC 1584
Db 1658 CGGGCAGTCCACCGGACCCCGGGGACACACACCCCGCCAGCCCGGGGTC 1717
Qy 1585 GGGGAGCGCGCTGAGGAGTCTCTCAACTCCATCCGCAACAGCTTCTGGGTCGCCCT 1644
Db 1718 GGGGAGCGCGCTGAGGAGTCTCTCAACTCCATCCGCAACAGCTTCTGGGTCGCCCT 1777
Qy 1645 CGCTTTCACCGCGCAAGATGAGTCCCTACCGTGGAGAGTCTCCAGCTTGACGCCA 1704
Db 1778 CGCTTTCACCGCGCAAGATGAGTCCCTACCGTGGAGAGTCTCCAGCTTGACGCCA 1837
Qy 1705 GAGTCTCTCCCGAGCTGGCAAAACGCTCCTGGTTTCGGGAACCTTCATCTCTTGACAAA 1764
Db 1838 GAGTCTCTCCCGAGCTGGCAAAACGCTCCTGGTTTCGGGAACCTTCATCTCTTGACAAA 1897
Qy 1765 GAAGAACAATAATCTCTGTTGTAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1824
Db 1898 GAAGAACAATAATCTCTGTTGTAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1957
Qy 1825 GTCCATGCTTTCTGTGATCCCGAGCTGAGTGCATGAGTGTCTGTACAGACAGCTTC 1884
Db 1958 GTCCATGCTTTCTGTGATCCCGAGCTGAGTGCATGAGTGTCTGTACAGACAGCTTC 2017
Qy 1885 AGGGCGGAGTACAGGAGTGGCGGCCCTCCGCTCTTCCAAAGCCCGCTCGCTTCAG 1944
Db 2018 AGGGCGGAGTACAGGAGTGGCGGCCCTCCGCTCTTCCAAAGCCCGCTCGCTTCAG 2077
Qy 1945 GTGGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGGAGCGGAGCGGAGGAGGT 2004
Db 2078 GTGGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGGAGCGGAGCGGAGGAGGT 2137
Qy 2005 GTGGGATCTACTCCGTCACTTCACTCTCATCTCGGGTCCCGAGCGCTGGTTCAGGCA 2064
Db 2138 GTGGGATCTACTCCGTCACTTCACTCTCATCTCGGGTCCCGAGCGCTGGTTCAGGCA 2197

Qy 2065 GTGGTGGAGACCATCCAGGCACAGTCTCTGAGCACTCATGACAGCCCTCGTTCAGGCC 2124
Db 2198 GTGGTGGAGACCATCCAGGCACAGTCTCTGAGCACTCATGACAGCCCTCGTTCAGGCC 2257
Qy 2125 CTGGCAGACGAGAGAACCGGGGCCAGACCCGGCTCTGTGTGCTCCACCCCGAGGCTG 2184
Db 2258 CTGGCAGACGAGAGAACCGGGGCCAGACCCGGCTCTGTGTGCTCCACCCCGAGGCTG 2317
Qy 2185 CAGCCCCCAGCCCGCGCCAGACCCAGAGCTGAGAGCTCTCCCGCGGAGGCCCCCC 2244
Db 2318 CAGCCCCCAGCCCGCGCCAGACCCAGAGCTGAGAGCTCTCCCGCGGAGGCCCCCC 2377
Qy 2245 AAGGACAAAGAGTCTCTGGCCACCAACGAGGCCCTCTGCGCTGA 2289
Db 2378 AAGGACAAAGAGTCTCTGGCCACCAACGAGGCCCTCTGCGCTGA 2422

RESULT 10
AAL55772
ID AAL55772 standard; cDNA; 2953 BP.
XX
AC AAL55772;
XX
DT 17-SEP-2003 (first entry)
XX
Human eukaryotic protein kinase 55053 cDNA.
XX
Cardiant; antianginal; antiarteriosclerotic; antidiabetic; thyromimetic;
XX
antiarrhythmic; cytostatic; nootropic; neuroprotective; antiparkinsonian;
XX
anticongulant; antidepressant; tranquiliser; antimigraine; EPK 55053;
XX
eukaryotic protein kinase; cellular growth disorder; angina; cancer;
XX
cognitive; neurodegenerative; Alzheimer's disease; learning; hormone;
XX
autonomic function; memory; neuropsychiatric; depression; reproductive;
XX
musculoskeletal; immune system; human; ss; gene.
XX
Homo sapiens.
XX
Key Location/Qualifiers
5'UTR 1..85
/tag= a
/note= "5, untranslated region"
CDS 86..2422
/tag= b
/product= "Human eukaryotic protein kinase 55053 protein"
3'UTR 2423..2953
/tag= c
/note= "3, untranslated region"
WO2003042371-A2.
XX
22-MAY-2003.
XX
15-NOV-2002; 2002WO-US036967.
XX
15-NOV-2001; 2001US-00003690.
XX
(MILL-) MILLENNIUM PHARM INC..
XX
Curtis RAJ;
XX
WPI; 2003-449574/42.
XX
P-PSDB; AAO3053.
XX
New isolated EPK-55053 nucleic acid and polypeptide, useful for
XX
diagnosing and treating EPK-55053-related disorders, such as
XX
hypertension, arteriosclerosis, myocardial infarction, diabetes mellitus,
XX
cancer and/or epilepsy.
XX
Claim 1; Fig 1A-1B; 86pp; English.
XX
The invention relates to a novel isolated nucleic acid molecule
XX
comprising a sequence which encodes a eukaryotic protein kinase (EPK) -
CC

55053 polypeptide. The polynucleotides and polypeptides of the invention may play a role as modulating agents in regulating a variety of cellular processes. Furthermore, the methods and compositions of the present invention may be useful during the diagnosis, screening and treatment of various disorders including cellular growth-related disorders such as angina and cancer, cognitive and neurodegenerative disorders e.g. Alzheimer's disease, autonomic function disorders, learning or memory disorders and neuropsychiatric disorders such as depression. In addition, disorders associated with the musculoskeletal, reproductive and immune systems, as well as disorders which are cardiac or hormone related, may be addressed by the present invention. The current sequence is that of the human EPK-55053 cDNA of the invention

XX Sequence 2953 BP; 609 A; 956 C; 878 G; 510 T; 0 U; 0 Other;

Query Match 88.3%; Score 2020.2; DB 9; Length 2953;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 265 TTTAGGTACCTGGTCTGGAGCAGTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 324
DB 398 TATTGTACCTGGTCTGGAGCAGTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 457
QY 325 AAGGGAGAGCTGACGCCCAAGAGAGGCCGAAAGTTCTTCGCCAGATTGTCTGCGCTG 384
DB 458 AAGGGAGAGCTGACGCCCAAGAGAGGCCGAAAGTTCTTCGCCAGATTGTCTGCGCTG 517
QY 385 GACTTCTGCCACAGCTACTTCATCTGCCACAGAGACCTTAAAGCCCGAGAACCTGCTTTTG 444
DB 518 GACTTCTGCCACAGCTACTTCATCTGCCACAGAGACCTTAAAGCCCGAGAACCTGCTTTTG 577
QY 445 GATGAGAAAAAACAATCATCGGATTCGAGCTTCGGGATGCGGTCCCTGCGAGTGGGGAC 504
DB 578 GATGAGAAAAAACAATCATCGGATTCGAGCTTCGGGATGCGGTCCCTGCGAGTGGGGAC 637
QY 505 AGCTCTCTGAGACCAAGTGGGGTCCCGCCATTCATGCGTGTCCAGAGGTGATTAAAGGG 564
DB 638 AGCTCTCTGAGACCAAGTGGGGTCCCGCCATTCATGCGTGTCCAGAGGTGATTAAAGGG 697
QY 565 GAAAAATATGATGGCCCGGGGAGAGATGTGGAGCTGTGGAGTCACTCTTCGCGCTG 624
DB 698 GAAAAATATGATGGCCCGGGGAGAGATGTGGAGCTGTGGAGTCACTCTTCGCGCTG 757
QY 625 CTGTGGGGGCTCTGCGCTTTGATGACAGCAAACTCCGCGAGCTGTGGAGAGGTGAAA 684
DB 758 CTGTGGGGGCTCTGCGCTTTGATGACAGCAAACTCCGCGAGCTGTGGAGAGGTGAAA 817
QY 685 CGGGGCTCTTCCACATGCCCACTTCACTTCCTCCAGATTGCCAGAGCTCTGAGGGGA 744
DB 818 CGGGGCTCTTCCACATGCCCACTTCACTTCCTCCAGATTGCCAGAGCTCTGAGGGGA 877
QY 745 ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAAATCCTTGG 804
DB 878 ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAAATCCTTGG 937
QY 805 TACTAGCGGGGAAACAGAGCCAGACCCGTGCTGGAGCCAGCCCTGCGCGCGGTGTA 864
DB 938 TACTAGCGGGGAAACAGAGCCAGACCCGTGCTGGAGCCAGCCCTGCGCGCGGTGTA 997
QY 865 GCCATGCGGAGCTGCCATCCACGGAGAGTGGACCCCGACGCTCTAGAGAGATGGCA 924
DB 998 GCCATGCGGAGCTGCCATCCACGGAGAGTGGACCCCGACGCTCTAGAGAGATGGCA 1057
QY 925 TCACTGGGCTGTCTCAGGGACCGGAGAGGCTGATCGCAGCTGCGCAGTGGAGGAG 984
DB 1058 TCACTGGGCTGTCTCAGGGACCGGAGAGGCTGATCGCAGCTGCGCAGTGGAGGAG 1117
QY 985 AACCAAGAAAGATGATATATTCTGCTTTTGGATCGGAGGAGCGGTATCCAGCTGT 1044
DB 1118 AACCAAGAAAGATGATATATTCTGCTTTTGGATCGGAGGAGCGGTATCCAGCTGT 1177
QY 1045 GAGGACAGAGACCTGCTCCCGGAATGATGTTGACCCCGCCCGGAAAGCGTGTGGATTCT 1104

DB 1178 GAGGACAGAGACCTGCTCCCGGAATGATGTTGACCCCGGAAAGCGTGTGGATTCT 1237
QY 1105 CCATGCTGAGCCGTACACGGAAAGCGCGACCGAGCGGAAGTCCATGGAAGTCTCTGAGC 1164
DB 1238 CCATGCTGAGCCGTACACGGAAAGCGCGACCGAGCGGAAGTCCATGGAAGTCTCTGAGC 1297
QY 1165 ATCACCAGTCCGGGGGTGGTGGCTCCCTCTGATACCCACCGAGCGGCTTTGGAGATGGCC 1224
DB 1298 ATCACCAGTCCGGGGGTGGTGGCTCCCTCTGATACCCACCGAGCGGCTTTGGAGATGGCC 1357
QY 1225 CAGCACAGCCAGAGATCCCGTACGCTCAGTGGAGCCCTCCACGGTCTGTCTCTCAGGCCCT 1284
DB 1358 CAGCACAGCCAGAGATCCCGTACGCTCAGTGGAGCCCTCCACGGTCTGTCTCTCAGGCCCT 1417
QY 1285 CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTTCACCCGAGCGGGGGTGGAGATGAG 1344
DB 1418 CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTTCACCCGAGCGGGGGTGGAGATGAG 1477
QY 1345 GCTCGAGGGGGGGCTCCCGACTTCCAAAAACGAGAGCTGCTTCTCGGGGGCCCGAGG 1404
DB 1478 GCTCGAGGGGGGGCTCCCGACTTCCAAAAACGAGAGCTGCTTCTCGGGGGCCCGAGG 1537
QY 1405 GGTGGGGGGCGCCGGGAGAGAGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCGGC 1464
DB 1538 GGTGGGGGGCGCCGGGAGAGAGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCGGC 1597
QY 1465 CCCCCAGGCTCCCGCGCTCTCTGCGGGAGACCCCTTGCACTGCGCTCTGCAACAGCC 1524
DB 1598 CCCCCAGGCTCCCGCGCTCTCTGCGGGAGACCCCTTGCACTGCGCTCTGCAACAGCC 1657
QY 1525 CGGGCAGTCCACCGGGAGACCCCGGGGAGAAACACACCCCGCCAGCCCGGGGGTGGCGTC 1584
DB 1658 CGGGCAGTCCACCGGGAGACCCCGGGGAGAAACACACCCCGCCAGCCCGGGTGGCGTC 1717
QY 1585 GGGGAGCGCCCTGGAGAGTCTCACTCCATCCGCAACAGCTTCCTGGGGTCCCT 1644
DB 1718 GGGGAGCGCCCTGGAGAGTCTCTCACTCCATCCGCAACAGCTTCCTGGGGTCCCT 1777
QY 1645 CGCTTTTACCGCGCGCAAGATGCAAGTCCCTTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1704
DB 1778 CGCTTTTACCGCGCGCAAGATGCAAGTCCCTTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1837
QY 1705 GAGTCTCTCCCGAGCTGGCAAAAACGCTCTGGTTTGGGAACTTCACTCTCTTGGGACAAA 1764
DB 1838 GAGTCTCTCCCGAGCTGGCAAAAACGCTCTGGTTTGGGAACTTCACTCTCTTGGGACAAA 1897
QY 1765 GAAGAAACAATATTTCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1824
DB 1898 GAAGAAACAATATTTCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1957
QY 1825 GTCCATGCTCTTCTGTGATCCCGCAGCTGAGTCAAGTGTGCTGTCAACAGCCAGCTTC 1884
DB 1958 GTCCATGCTCTTCTGTGATCCCGCAGCTGAGTCAAGTGTGCTGTCAACAGCCAGCTTC 2017
QY 1885 AGGGCCGAGTACAAAGCCAGTGGCGGCCCTCTCGTCTTCCAAAAGCCCGTCCGCTTCAG 1944
DB 2018 AGGGCCGAGTACAAAGCCAGTGGCGGCCCTCTCGTCTTCCAAAAGCCCGTCCGCTTCAG 2077
QY 1945 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGAGGT 2004
DB 2078 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGAGGT 2137
QY 2005 GGTGGGATCTTACTCCGCTCACTTTCACTCTCATCTCGGGTCCAGCCGCTCGGTTCAAGCGA 2064
DB 2138 GGTGGGATCTTACTCCGCTCACTTTCACTCTCATCTCGGGTCCAGCCGCTCGGTTCAAGCGA 2197
QY 2065 GTGGTGGAGACCATTCAGGACAGCTCTCTGAGCACTCATGACAGGCCCTCCGTCGAGGCC 2124
DB 2198 GTGGTGGAGACCATTCAGGACAGCTCTCTGAGCACTCATGACAGGCCCTCCGTCGAGGCC 2257
QY 2125 CTGGCAGACGAGAAAGAAAGGGGGCCAGACCCGGGCTGTGGTGCCTCCACCCCGAGCGCTG 2184
DB 2258 CTGGCAGACGAGAAAGAAAGGGGGCCAGACCCGGGCTGTGGTGCCTCCACCCCGAGCGCTG 2317

QY 2185 CAGCCCCCACCAGCCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCGCCCCC 2244
DB 2318 CAGCCCCCACCAGCCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCGCCCCC 2377
QY 2245 AAGGACAAAGTCTCTGGCCACCAAGGAGACCCCTCTGGCCCTGA 2289
DB 2378 AAGGACAAAGTCTCTGGCCACCAAGGAGACCCCTCTGGCCCTGA 2422

RESULT 11

ID ADE38430 standard; DNA; 2980 BP.

AC ADE38430;

XX 29-JAN-2004 (first entry)

XX Human protein 68862 gene sequence.

XX tumorigenic disorder; angiogenic disorder; aberrant gene expression;
XX aberrant protein activity; cytostatic; antithyroid; antidiabetic;
KW ophthalmological; cancer; breast cancer; colon cancer; lung cancer;
KW prostatic cancer; Grave's disease; diabetic retinopathy; gene; ds;
protein 68862.

XX Homo sapiens.

XX Location/Qualifiers

XX 86..2422

FT CDS /*tag= a

FT /product= "Human protein 68862"

XX WO2003065006-A2.

XX 07-AUG-2003.

XX 30-JAN-2003; 2003WO-US002588.

XX 31-JAN-2002; 2002US-0353600P.

XX 15-MAR-2002; 2002US-0364517P.

XX 09-APR-2002; 2002US-0371075P.

XX 10-APR-2002; 2002US-0371507P.

XX 16-APR-2002; 2002US-0372984P.

XX 19-APR-2002; 2002US-0374194P.

XX 24-MAY-2002; 2002US-0382995P.

XX 31-MAY-2002; 2002US-0385023P.

XX 14-JUN-2002; 2002US-0388853P.

XX 17-JUN-2002; 2002US-0389395P.

XX 25-JUN-2002; 2002US-0391324P.

XX 15-JUL-2002; 2002US-0395944P.

XX 22-JUL-2002; 2002US-0397726P.

XX 13-AUG-2002; 2002US-0403046P.

XX 22-AUG-2002; 2002US-0405155P.

XX 27-AUG-2002; 2002US-0406361P.

XX 25-OCT-2002; 2002US-0421195P.

XX 12-NOV-2002; 2002US-0425456P.

XX 19-NOV-2002; 2002US-0427626P.

XX 10-DEC-2002; 2002US-0432122P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hunter JJ, Macbeth KJ, Tsai F, Lesoon A, Lightcap ES;

PI Williamson MW, Rudolph-Owen LA;

XX WPI; 2003-646176/61.

DR P-PSDB; ADE38431.

XX Treating subject having tumorigenic disorder or angiogenic disorder
PT created by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic
PT acid, by administering a modulator.

XX Disclosure; SEQ ID NO 91; 454pp; English.

XX

CC This invention relates to a novel method of treating a human subject
CC having a tumorigenic disorder or angiogenic disorder, caused by aberrant
CC gene expression or activity of an isolated protein, by administering a
CC modulator. The modulator may have cytostatic, antithyroid, antidiabetic
CC or ophthalmological activity. The method is useful for treating a subject
CC having a tumorigenic or angiogenic disorder, in particular for treating
CC cancer (for example breast cancer, colon cancer, lung cancer or prostatic
CC cancer) and, for example, Grave's disease and diabetic retinopathy. The
CC present sequence is a DNA sequence which encodes the novel isolated human
CC protein 68862 of the invention.

SQ Sequence 2980 BP; 625 A; 959 C; 886 G; 510 T; 0 U; 0 Other;

Query Match 88.3%; Score 2020.2; DB 10; Length 2980;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 265 TTTAGTACTGGTTCTGGAGCACGCTCTCGGGGGTGAGCTATTGCACTACCTGGTAAAG 324

DB 398 TATTTGTACTGGTTCTGGAGCACGCTCTCGGGGGTGAGCTATTGCACTACCTGGTAAAG 457

QY 325 AAGGGGAGACTGACGCGCCCAAGGAGGCCGAAAGTTCTTCCGCCAGATTGTCTGCGCTG 384

DB 458 AAGGGGAGACTGACGCGCCCAAGGAGGCCGAAAGTTCTTCCGCCAGATTGTCTGCGCTG 517

QY 385 GACTTCTGCCACAGCTACTTCCATCTGCCACAGAGACTAAAGCCCGAGAACCTGCTTTTG 444

DB 518 GACTTCTGCCACAGCTACTTCCATCTGCCACAGAGACTAAAGCCCGAGAACCTGCTTTTG 577

QY 445 GATGAGAAAAACACATCCGATTGCGACTTCGGCATGCGCTCCCTGAGGTGGGGGAC 504

DB 578 GATGAGAAAAACACATCCGATTGCGACTTCGGCATGCGCTCCCTGAGGTGGGGGAC 637

QY 505 AGCTCTCTGGAGACACAGCTGCGGGTCCCCCATTTATGCGTGTCCAGAGTGATTAAGGGG 564

DB 638 AGCTCTCTGGAGACACAGCTGCGGGTCCCCCATTTATGCGTGTCCAGAGTGATTAAGGGG 697

QY 565 GAAAAATATGATGCGCGCGGGCAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTG 624

DB 698 GAAAAATATGATGCGCGCGGGCAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTG 757

QY 625 CTGCTGGGGCTCTGCGCTTTGATGACGACAACTCCGCCAGCTGTGGAGAGGTGAAA 684

DB 758 CTGCTGGGGCTCTGCGCTTTGATGACGACAACTCCGCCAGCTGTGGAGAGGTGAAA 817

QY 685 CGGGGGCTCTTCCACATGCCCCACTTCACTTCTCCAGATTGCCAGAGCTCTCTGAGGGGA 744

DB 818 CGGGGGCTCTTCCACATGCCCCACTTCACTTCTCCAGATTGCCAGAGCTCTCTGAGGGGA 877

QY 745 ATGATCGAAGTGAGCGCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG 804

DB 878 ATGATCGAAGTGAGCGCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG 937

QY 805 TACCTAGCGGGGAAACACAGCCAGACCCGCTGCTGGAGCAGCCCTGCGCCGCGGTA 864

DB 938 TACCTAGCGGGGAAACACAGCCAGACCCGCTGCTGGAGCAGCCCTGCGCCGCGGTA 997

QY 865 GCCATGCGGAGCCCTGCCATCCAAACGGAGAGCTGGACCCCGACGTCCTTAGAGAGATGGCA 924

DB 998 GCCATGCGGAGCCCTGCCATCCAAACGGAGAGCTGGACCCCGACGTCCTTAGAGAGATGGCA 1057

QY 925 TCCTGGGCTGCTTCCAGGACCCGAGAGAGCTGATCGGAGCTGCGCAGTGGAGGAG 984

DB 1058 TCCTGGGCTGCTTCCAGGACCCGAGAGAGCTGATCGGAGCTGCGCAGTGGAGGAG 1117

QY 985 AACCAAGAAAAAGATGATATATTCTCTTTTGGATCGGAAGAGCGGCTATCCAGCTGT 1044

DB 1118 AACCAAGAAAAAGATGATATATTCTCTTTTGGATCGGAAGAGCGGCTATCCAGCTGT 1177

QY 1045 GAGGACCAAGACCTGCTCCCGGAATGATGTTGACCCCCCGGAAACGCTGTGGATTCT 1104

DB 1178 GAGGACCAAGACCTGCTCCCGGAATGATGTTGACCCCCCGGAAACGCTGTGGATTCT 1237

QY 1105 CCCATGCTGAGCGCTCAGCGAAGGGGCGACGAGCGGAGTCCATGGAAGTCTCTGAGC 1164
Db 1338 CCCATGCTGAGCGCTCAGCGAAGGGGCGACGAGCGGAGTCCATGGAAGTCTCTGAGC 1297
QY 1165 ATCAACCATGCGGGGGTGGTGGCTCCCTGTACCCACCGAGCGGGCTTGGAGATGGCC 1234
Db 1298 ATCAACCATGCGGGGGTGGTGGCTCCCTGTACCCACCGAGCGGGCTTGGAGATGGCC 1357
QY 1225 CAGCACGACGAGATCCCGTAGCGTCACTGAGGAGCTCCACGGGTCTGTCTCCAGCCCT 1284
Db 1358 CAGCACGACGAGATCCCGTAGCGTCACTGAGGAGCTCCACGGGTCTGTCTCCAGCCCT 1417
QY 1285 CTRAGACGACGAGGAGTCCGGTCTTTTCTTTTCAAGGAGCGGGGCTGGAGATGAG 1344
Db 1418 CTAAGACGACGAGGAGTCCGGTCTTTTCTTTTCAAGGAGCGGGGCTGGAGATGAG 1477
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Db 1478 GCTCAGGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTTCTCGGGGCGCCAGG 1537
QY 1405 GGTGGGCGCGCGGAGAGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCGC 1464
Db 1538 GGTGGGCGCGCGGAGAGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCGC 1597
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Db 1598 CCCCAGGCTCCCGCGCTCTCTGGGAGAGCCCGCTTGAAGTCTGACACGCGCC 1657
QY 1525 CGGCGAGTCCACCGGAGCCCGGGGACACACACCCCGCCAGCGCGGGGGGTC 1584
Db 1658 CGGCGAGTCCACCGGAGCCCGGGGACACACACCCCGCCAGCGCGGGGGTC 1717
QY 1585 GGGGAGCGCGCTGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTGGGCTCCCT 1644
Db 1718 GGGGAGCGCGCTGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTGGGCTCCCT 1777
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Db 1778 CGCTTTCAGCGGCGAGATGAGTGTCTTACCGCTGAGGAGTGTCTGAGTGTGACGCCA 1837
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QY 1765 GAGAACAAATATTCCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGATC 1824
Db 1898 GAGAACAAATATTCCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGATC 1957
QY 1825 GTCCATGCTTCTGTGCTGATCCCGAGCTGAGTCAAGTGTGTGTGTCACAGCAGGTTT 1884
Db 1958 GTCCATGCTTCTGTGCTGATCCCGAGCTGAGTCAAGTGTGTGTGTCACAGCAGGTTT 2017
QY 1885 AGGCGCAGTACAGGCGAGTGGCGGCGCTTCCGCTTCCAAAGCGCGTCCGCTCCAG 1944
Db 2018 AGGCGCAGTACAGGCGAGTGGCGGCGCTTCCGCTTCCAAAGCGCGTCCGCTCCAG 2077
QY 1945 GTGACATCAGCTCTCTGAGGGTTCAGAGCGCTTCCCGGAGCGGAGCGGAGGT 2004
Db 2078 GTGACATCAGCTCTCTGAGGGTTCAGAGCGCTTCCCGGAGCGGAGCGGAGGT 2137
QY 2005 GGTGGCATCTACTCCGTCACTTCACTCTCATCTCGGGTCCAGCGGTTCAAGCGA 2064
Db 2138 GGTGGCATCTACTCCGTCACTTCACTCTCATCTCGGGTCCAGCGGTTCAAGCGA 2197
QY 2065 GTGTGAGACCATTCAGGACAGCTCTGTGAGCACTCATGACAGCGCTTCCGTCAGGCC 2124
Db 2198 GTGTGAGACCATTCAGGACAGCTCTGTGAGCACTCATGACAGCGCTTCCGTCAGGCC 2257
QY 2125 CTGCGACAGGAGAAACGGGGGCGCCAGACCGGCGCTGTGTGTCGCCACCGGAGCGCTG 2184
Db 2258 CTGCGACAGGAGAAACGGGGGCGCCAGACCGGCGCTGTGTGTCGCCACCGGAGCGCTG 2317

QY 2185 CAGCCCCCAGCCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGAGGCCCCCCC 2244
Db 2318 CAGCCCCCAGCCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGAGGCCCCCCC 2377
QY 2245 AAGGACAAAGAGTCTCTGGCCACCAACGAGGACCCCTCTGCGCTGA 2289
Db 2378 AAGGACAAAGAGTCTCTGGCCACCAACGAGGACCCCTCTGCGCTGA 2422
RESULT 12
ID ADL14127
XX ADL14127 standard; cDNA; 2980 BP.
AC ADL14127;
XX
DT 17-JUN-2004 (first entry)
XX
DE Novel human gene 55053 cDNA.
XX
KW cytosolic; cardiant; hypotensive; antiangiinal; osteopathic;
KW antiarthritic; antirheumatic; neuroprotective; antiinflammatory;
KW antipsoriatic; antihistaminic; cardiovascular; virucide; analgesic; CNS;
KW angiogenesis inhibitor; angiogenesis stimulator; cerebroprotective;
KW nephrotropic; antithyroid; dermatological; immunomodulator;
KW cell proliferation disorder; cell differentiation disorder;
KW brain disorder; platelet disorder; breast disorder; colon disorder;
KW kidney disorder; renal disorder; lung disorder; ovarian disorder;
KW prostate disorder; cervical disorder; spleen disorder; thymus disorder;
KW thyroid disorder; testes disorder; haematopoietic disorder;
KW pancreatic disorder; skeletal muscle disorder; skin disorder;
KW dermal disorder; bone metabolism disorder; immune disorder;
KW inflammatory disorder; cardiovascular disorder;
KW endothelial cell disorder; liver disorder; viral disease; pain disorder;
KW metabolic disorder; neurological disorder;
KW central nervous system disorder; erythroid disorder;
KW blood vessel disorder; angiogenic disorder; cancer; heart failure;
KW hypertension; angina; osteoarthritis; rheumatoid arthritis;
KW multiple sclerosis; Crohn's disease; psoriasis; asthma;
KW cell proliferation; cell differentiation; cell growth; cell division;
KW human; gene; ss.
XX
OS Homo sapiens.
XX
PN US2004058355-A1.
XX
PD 25-MAR-2004.
XX
PF 25-APR-2003; 2003US-00423543.
XX
PR 30-SEP-1998; 98US-00163821.
PR 27-JAN-1999; 99US-0117580P.
PR 25-MAR-1999; 99US-00276400.
PR 30-JUL-1999; 99US-00365162.
PR 09-SEP-1999; 99US-00392189.
PR 05-OCT-1999; 99US-00412210.
PR 23-NOV-1999; 99US-00448076.
PR 29-FEB-2000; 2000US-0186061P.
PR 28-APR-2000; 2000US-0200688P.
PR 19-MAY-2000; 2000US-0205447P.
PR 30-JUN-2000; 2000US-00608921.
PR 31-JUL-2000; 2000US-0221925P.
PR 25-SEP-2000; 2000US-0234922P.
PR 25-SEP-2000; 2000US-0235035P.
PR 08-NOV-2000; 2000US-0246669P.
PR 09-NOV-2000; 2000US-00711216.
PR 14-NOV-2000; 2000US-0248325P.
PR 15-NOV-2000; 2000US-0248893P.
PR 22-DEC-2000; 2000US-0257511P.
PR 05-JAN-2001; 2001US-0260166P.
PR 28-FEB-2001; 2001US-00797039.
PR 27-APR-2001; 2001US-00845044.
PR 20-JUL-2001; 2001US-00909743.
PR 31-JUL-2001; 2001US-00920346.

PR	13-AUG-2001;	2001US-00928531.	
PR	14-AUG-2001;	2001US-00929218.	
PR	15-AUG-2001;	2001US-0312539P.	
PR	25-SEP-2001;	2001US-00963159.	
PR	08-NOV-2001;	2001US-00080816.	
PR	13-NOV-2001;	2001US-00012055.	
PR	15-NOV-2001;	2001US-00003690.	
PR	30-JAN-2002;	2002US-00060763.	
PR	25-MAR-2002;	2002US-00105989.	
PR	12-APR-2002;	2002US-00121911.	
PR	12-AUG-2002;	2002US-00217168.	
PR	22-OCT-2002;	2002US-00278036.	
PR	02-JAN-2003;	2003US-00336489.	
PR	03-JAN-2003;	2003US-00336153.	
XX	(MILL-) MILLENNIUM PHARM INC.		
XX			
XX	Kapeller-Libermann R, Hunter JU, Meyers RE, Rudolph-Owen LA;		
PI	Curtis RAJ, Olandt PU, Tsai F, Galvin KM, Chun M, Williamson MJ;		
PI	Silos-Santiago I, Bandaru R;		
XX			
DR	WPI; 2004-268798/25.		
DR	P-PSDB; ADL14128.		
XX			
PT	New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529,		
PT	26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593		
PT	nucleic acid molecules and proteins, useful for treating, e.g. cancer,		
PT	heart failure and angina.		
XX			
PS	Claim 1; SEQ ID NO 10; 139pp; English.		
XX			
CC	The invention describes an isolated 21910, 56634, 55053, 2504, 15977,		
CC	14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217,		
CC	21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising		
CC	any one of 40 nucleotide sequences (I). The nucleic acid molecules and		
CC	polypeptides are useful for diagnosing and treating a subject having a		
CC	disorder, or a subject at risk of developing a disorder, which is		
CC	associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501,		
CC	17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983,		
CC	m1983, 38555 or 593 activity, such as cellular proliferative and/or		
CC	differentiative disorders, brain disorders, platelet disorders, breast		
CC	disorders, colon disorders, kidney (renal) disorders, lung disorders,		
CC	ovarian disorders, prostate disorders, cervical disorders, spleen		
CC	disorders, thymus disorders, thyroid disorders, testes disorders,		
CC	hematopoietic disorders, pancreatic disorders, skeletal muscle disorders,		
CC	skin (dermal) disorders, disorders associated with bone metabolism,		
CC	immune, e.g. inflammatory disorders, cardiovascular disorders,		
CC	endothelial cell disorders, liver disorders, viral diseases, pain		
CC	disorders, metabolic disorders, neurological or central nervous system		
CC	disorders, erythroid disorders, blood vessel disorders or angiogenic		
CC	disorders (all claimed), e.g. cancer, heart failure, hypertension,		
CC	angina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, Crohn's		
CC	disease, psoriasis, or asthma. The nucleic acid molecules and		
CC	polypeptides are also useful as modulating agents in regulating a variety		
CC	of cellular processes, e.g. cell proliferation, differentiation, growth and		
CC	division. This sequence encodes a novel human protein of the invention.		
CC	Note: The sequences given in the specification are also available in		
CC	electronic format from		
CC	ftp.seqdata.uspco.gov/sequence.html?DocID=20040058355.		
XX			
SQ	Sequence 2980 BP; 625 A; 959 C; 886 G; 510 T; 0 U; 0 Other;		
	Query Match 88.3%; Score 2020.2; DB 12; Length 2980;		
	Best Local Similarity 99.9%; Pred. No. 0;		
	Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
QY	265 TTTAGGTACCTGGTCTCGAGACGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 324		
Db	398 TATTGTGTACCTGGTCTCGAGACGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 457		
QY	325 AAGGGAGACTGACGCCCAAGGAGGCCGGAAGTTCTTCGCCAGATTGTGTCTGGCGCTG 384		
Db	458 AAGGGGAGACTGACGCCCAAGGAGGCCGGAAGTTCTTCGCCAGATTGTGTCTGGCGCTG 517		

QY	385 GACTTCTGCCACAGCTATTCCATCTGTGCCACAGAGACCTTAAAGCCCGAGAACCTGCTTTTG 444	
Db	518 GACTTCTGCCACAGCTATTCCATCTGTGCCACAGAGACCTTAAAGCCCGAGAACCTGCTTTTG 577	
QY	445 GATGAGAAAAACAATCCGCAATTCGAGACTTCGGCATCGCGTCCCTGAGGTGGGGGAC 504	
Db	578 GATGAGAAAAACAATCCGCAATTCGAGACTTCGGCATCGCGTCCCTGAGGTGGGGGAC 637	
QY	505 AGCCTCTCGAGACACAGCTCGGGTCCCGCCCATTTATGCGTGTCCAGAGGTGATTAAAGGG 564	
Db	638 AGCCTCTCGAGACACAGCTCGGGTCCCGCCCATTTATGCGTGTCCAGAGGTGATTAAAGGG 697	
QY	565 GAAAAATATGATGGCCCGCGGCAGACATGTGGAGCTGTGGAGTCACTCTTCCTCGCCCTG 624	
Db	698 GAAAAATATGATGGCCCGCGGCAGACATGTGGAGCTGTGGAGTCACTCTTCCTCGCCCTG 757	
QY	625 CTCGTGGGGGCTCTGCGCTTTTGAATGACGACACATCCCGCAGCTGTGGAGAGGTGAAA 684	
Db	758 CTCGTGGGGGCTCTGCGCTTTTGAATGACGACACATCCCGCAGCTGTGGAGAGGTGAAA 817	
QY	685 CGGGGGCTCTCCACATGCCCCACATTTCTTCCAGATTGCCAGAGCCTCTCGAGGGGA 744	
Db	818 CGGGGGCTCTTCCACATGCCCCACATTTCTTCCAGATTGCCAGAGCCTCTCGAGGGGA 877	
QY	745 ATGATCGAAGTGGAGCCCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAACATCTTGG 804	
Db	878 ATGATCGAAGTGGAGCCCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAACATCTTGG 937	
QY	805 TACCTAGGCGGGAAAAACAAGCAGACACCGGTGCTGGAGCAGCCCTCGCGCCGGGTA 864	
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QY	865 GCATCGCGAGCTGCTCATCAACGAGAGCTGGACCCCGAGCTCTTAGAGAGCATGGCA 924	
Db	998 GCATCGCGAGCTGCTCATCAACGAGAGCTGGACCCCGAGCTCTTAGAGAGCATGGCA 1057	
QY	925 TCATCGGGTGTCTTACGGGACCGCGAGAGGCTGCATCGCGAGTGCAGTGAAGGAG 984	
Db	1058 TCATCGGGTGTCTTACGGGACCGCGAGAGGCTGCATCGCGAGTGCAGTGAAGGAG 1117	
QY	985 AACCAAGAAAAAGATGATATATATCTGCTTTTGGATCGAAGAGCGGTATCCAGCTGT 1044	
Db	1118 AACCAAGAAAAAGATGATATATATCTGCTTTTGGATCGAAGAGCGGTATCCAGCTGT 1177	
QY	1045 GAGGACACGAGCTGCTCTCCCGGAATGATTTGACCCCGGAGCGGTGTGGATTCT 1104	
Db	1178 GAGGACACGAGCTGCTCTCCCGGAATGATTTGACCCCGGAGCGGTGTGGATTCT 1237	
QY	1105 CCATGCTGAGCCGCTCACGGGAAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1164	
Db	1238 CCATGCTGAGCCGCTCACGGGAAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1297	
QY	1165 ATCACCAGTCCCGGGGGTGTGCTCCCTGTATCCACCGAGCGGGCTTGGAGATGGCC 1224	
Db	1298 ATCACCAGTCCCGGGGGTGTGCTCCCTGTATCCACCGAGCGGGCTTGGAGATGGCC 1357	
QY	1225 CAGCAGACACAGATCCCGTAGCGTCACTGGAGCCTCCACGGGTCTGTCTCCAGCCCT 1284	
Db	1358 CAGCAGACACAGATCCCGTAGCGTCACTGGAGCCTCCACGGGTCTGTCTCCAGCCCT 1417	
QY	1285 CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTCAACCGAGCCGGGGGTGGAGATGAG 1344	
Db	1418 CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTCAACCGAGCCGGGGGTGGAGATGAG 1477	
QY	1345 GCTCGAGGGGGGGCTCCCGAGCTTCCAAAAACGACAGCGTGCCTTCTCGGGGGCCCCAGG 1404	
Db	1478 GCTCGAGGGGGGGCTCCCGAGCTTCCAAAAACGACAGCGTGCCTTCTCGGGGGCCCCAGG 1537	
QY	1405 GGTGGGGGGCGCGGGGAGAGAGCCCGCCCGCCCGAGTCCCGCTCCACACCCCTGCCCGGC 1464	
Db	1538 GGTGGGGGGCGCGGGGAGAGAGCCCGCCCGCCCGAGTCCCGCTCCACACCCCTGCCCGGC 1597	

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QY 1465 CCCCAGGCTCCCGCGCTCTCTGGGGGAGACCCCTTGCACTCGCCTCTGCACACGCC 1524
Db 1598 CCCCAGGCTCCCGCGCTCTCTGGGGGAGACCCCTTGCACTCGCCTCTGCACACGCC 1657
QY 1525 CGGCGCAGTCCACCGGAGCCCGGGGACACACACACCCCGCGCGGTGGGGTTC 1584
Db 1658 CGGCGCAGTCCACCGGAGCCCGGGGACACACACACCCCGCGCGGTGGGGTTC 1717
QY 1585 GGGGAGCGCGCTGGAGAGTGTCTCAATCTCATTCGCAACAGCTTCTGGGCTCCCT 1644
Db 1718 GGGGAGCGCGCTGGAGAGTGTCTCAATCTCATTCGCAACAGCTTCTGGGCTCCCT 1777
QY 1645 CGCTTTTCCACCGGCAAGATGACGCTCCCTACCGCTGAGGAGATGTCAGCTTGACGCCA 1704
Db 1778 CGCTTTTCCACCGGCAAGATGACGCTCCCTACCGCTGAGGAGATGTCAGCTTGACGCCA 1837
QY 1705 GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTCGGGAATTCATCTCTTGCAAAA 1764
Db 1838 GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTCGGGAATTCATCTCTTGCAAAA 1897
QY 1765 GAAGAACAAATATTTCTGTGCTTAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1824
Db 1898 GAAGAACAAATATTTCTGTGCTTAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1957
QY 1825 GTCCATGCTTCTGTGATCCCGCAGCTGAGTCACAGTGTGCTGCACAGCAGCTTC 1884
Db 1958 GTCCATGCTTCTGTGATCCCGCAGCTGAGTCACAGTGTGCTGCACAGCAGCTTC 2017
QY 1885 AGGCCGAGTACAGGCGCAGTGGCGGCGCTCTCTTCAAAAGCCGCTCCGCTTCAG 1944
Db 2018 AGGCCGAGTACAGGCGCAGTGGCGGCGCTCTCTTCAAAAGCCGCTCCGCTTCAG 2077
QY 1945 GTGACATCAGCTCTCTGAGGCTCCAGAGCCCTTCCCGGACGCGGACGCGGAGGT 2004
Db 2078 GTGACATCAGCTCTCTGAGGCTCCAGAGCCCTTCCCGGACGCGGACGCGGAGGT 2137
QY 2005 GGTGGCATCTACTCGGTCACTTCACTCTCATCTCGGGTCCAGCGCTCGGTTCAGCGA 2064
Db 2138 GGTGGCATCTACTCGGTCACTTCACTCTCATCTCGGGTCCAGCGCTCGGTTCAGCGA 2197
QY 2065 GTGTGGAGACCATCTCAGGACACGCTCTGAGCACTCATGACACGCTCCGTCGACGCC 2124
Db 2198 GTGTGGAGACCATCTCAGGACACGCTCTGAGCACTCATGACACGCTCCGTCGACGCC 2257
QY 2125 CTGCGACAGCAGAGAAACGGGGCCCGACACCGGCTCTGCTGCTCCCGACCCCGAGCTG 2184
Db 2258 CTGCGACAGCAGAGAAACGGGGCCCGACACCGGCTCTGCTGCTCCCGACCCCGAGCTG 2317
QY 2185 CAGCCCCCAGCGCGCCGACGACGCTGAGTGTGAGTGTCTCCCGCGGAGGCCCGCC 2244
Db 2318 CAGCCCCCAGCGCGCCGACGACGCTGAGTGTGAGTGTCTCCCGCGGAGGCCCGCC 2377
QY 2245 AAGGACAAAGAGCTCTTGGCCCAACCAAGCGGACCCCTCTGCGCTCA 2289
Db 2378 AAGGACAAAGAGCTCTTGGCCCAACCAAGCGGACCCCTCTGCGCTCA 2422
```

RESULT 13

ADQ85869

ID ADQ85869 standard; cDNA; 2980 BP.

XX ADQ85869;

AC ADQ85869;

DT 07-OCT-2004 (first entry)

XX Human tumour-associated antigenic target (TAT) cDNA sequence #2741.

XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.

OS Homo sapiens.

XX W02004060270-A2.

PN

XX 22-JUL-2004.

XX 15-OCT-2003; 2003WO-US029126.

XX 18-OCT-2002; 2002US-0418988P.

XX (BETH) GENENTECH INC.

XX (WUTD/) WU T D.

XX (ZHOU/) ZHOU Y.

XX Wu TD, Zhou Y;

XX WPI; 2004-534300/51.

XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
XX preventing or treating cell proliferative disorders such as cancer.

XX Claim 1; SEQ ID NO 2741; 5504pp; English.

XX The present invention describes an isolated tumour-associated antigenic
XX target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
XX sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
XX (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
XX sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
XX nucleic acid; (2) a host cell comprising the above expression vector; (3)
XX a process for producing a polypeptide; (4) an isolated polypeptide
XX comprising: (a) an amino acid sequence encoded by any of the above
XX nucleotide sequences; (b) an amino acid sequence encoded by the full-
XX length coding region of the above nucleotide sequences; or (c) a sequence
XX having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
XX comprising the above polypeptide fused to a heterologous polypeptide; (6)
XX an isolated antibody that binds to the above polypeptide; (7) a process
XX for producing the antibody; (8) an isolated oligopeptide that binds to
XX the above polypeptide; (9) a tumour-associated antigenic target (TAT)
XX binding organic molecule that binds to the above polypeptide; (10) a
XX composition of matter comprising the above (chimeric) polypeptide,
XX antibody, oligopeptide or TAT binding organic molecule, in combination
XX with a carrier; (11) an article of manufacture comprising a container and
XX the composition of matter contained within the container; (12) methods of
XX inhibiting the growth of a cell that expresses the above protein, where
XX the growth of the cell is at least in part dependent upon a growth
XX potentiating effect of the above protein; (13) a method of
XX therapeutically treating a mammal having a cancerous tumour comprising
XX cells that express the above protein; (14) a method of determining the
XX presence of a protein in a sample suspected of containing the protein
XX described above; (15) methods of diagnosing the presence of a tumour in a
XX mammal; (16) a method for treating or preventing a cell proliferative
XX disorder associated with increased expression or activity of the above
XX protein; and (17) a method of binding an antibody, oligopeptide or
XX organic molecule to a cell that expresses the protein described above.
XX The TAT sequences have cytostatic activities, and can be used in gene
XX therapy. The composition and methods are useful for diagnosing,
XX preventing or treating cancer. The composition is also useful for preparing
XX a medicament for the therapeutic treatment or diagnostic detection of a
XX cell proliferative disorder or cancer. The present sequence represents a
XX human TAT cDNA sequence from the present invention.

XX Sequence 2980 BP; 607 A; 939 C; 909 G; 525 T; 0 U; 0 Other;

XX Query Match 88.3%; Score 2020.2; DB 13; Length 2980;

XX Best Local Similarity 99.9%; Pred. No. 0;

XX Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 265 TTTAGGTACTGTTCTGGAGCAGCTCTCGGGGGTGGAGCTATTCGACTACTGTTAAG 324

Db 491 TATTGTGTTACTGTTCTGGAGCAGCTCTCGGGGGTGGAGCTATTCGACTACTGTTAAG 550

QY 325 AAGGGAGACTGACGCCCAAGGAGGCCCGAAAGTTCTTCCGCCAGATTGTGTGCGCTG 384

Db 551 AAGGGAGACTGACGCCCAAGGAGGCCCGAAAGTTCTTCCGCCAGATTGTGTGCGCTG 610

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QY 385 GACTCTGCGACAGCTACTCCATCTGCCACAGAGACTTAAGCCCGAGAACCTGCTTTTG 444
Db |||||
QY 611 GACTTCTGCGACAGCTACTCCATCTGCCACAGAGACTTAAGCCCGAGAACCTGCTTTTG 670
Db |||||
QY 445 GATGAGAAAAAACAATCCGCAATTCCGCACTTCGGCATCGCTCCCTGCGAGGTGGGGAC 504
Db |||||
QY 671 GATGAGAAAAAACAATCCGCAATTCCGCACTTCGGCATCGCTCCCTGCGAGGTGGGGAC 730
QY 505 AGCTCTCTGAGACACAGCTGCGGGTCCGCCATATATGCGTGTCCAGAGGTATTAAGGGG 564
Db |||||
QY 731 AGCTCTCTGAGACACAGCTGCGGGTCCGCCATATATGCGTGTCCAGAGGTATTAAGGGG 790
QY 565 GAAAAATATCATGCGCGCGCGGAGACATGTGAGCTGTGGAGTCACTCTCTTCGCCCTG 624
Db |||||
QY 791 GAAAAATATGATGCGCGCGGAGACATGTGAGCTGTGGAGTCACTCTCTTCGCCCTG 850
QY 625 CTCGTGGGGCTCTGCCCTTTGATGACGACAACTCCGCGAGCTGTGAGAAAGGTGAAA 684
Db |||||
QY 851 CTCGTGGGGCTCTGCCCTTTGATGACGACAACTCCGCGAGCTGTGAGAAAGGTGAAA 910
QY 685 CGGGGCTCTTCCACATGCCCACTTTCATCTCCAGATTGCCAGAGCTCCTGAGGGGA 744
Db |||||
QY 911 CGGGGCTCTTCCACATGCCCACTTTCATCTCCAGATTGCCAGAGCTCCTGAGGGGA 970
QY 745 ATGATCGAAGTGGAGCCGCAAAAAGGCTCAGTCTGGAGCAAAATTGAGAAACATCTTTG 804
Db |||||
QY 971 ATGATCGAAGTGGAGCCGCAAAAAGGCTCAGTCTGGAGCAAAATTGAGAAACATCTTTG 1030
QY 805 TACTAGCGGGGAACACGAGCGACAGCCCGTGTCTGAGGACGAGCCCTGCGCCCGGGTA 864
Db |||||
QY 1031 TACTAGCGGGGAACACGAGCGACAGCCCGTGTCTGAGGACGAGCCCTGCGCCCGGGTA 1090
QY 865 GCCATCGGAGCCCTGCCATCCACGAGAGCTGAGCCCGGACGCTCTAGAGAGCATGGCA 924
Db |||||
QY 1091 GCCATCGGAGCCCTGCCATCCACGAGAGCTGAGCCCGGACGCTCTAGAGAGCATGGCA 1150
QY 925 TCACTGGGCTGCTTCAGGAGCCGCGAGAGGCTGCATCGGAGTGCAGTGGAGGAGAG 984
Db |||||
QY 1151 TCACTGGGCTGCTTCAGGAGCCGCGAGAGGCTGCATCGGAGTGCAGTGGAGGAGAG 1210
QY 985 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAGAGCGGTATCCAGCTGT 1044
Db |||||
QY 1211 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAGAGCGGTATCCAGCTGT 1270
QY 1045 GAGGACACGAGACCTGCTCCCGGAATGATGTTGACCCCGGAAAGCGTGTGGATTCT 1104
Db |||||
QY 1271 GAGGACACGAGACCTGCTCCCGGAATGATGTTGACCCCGGAAAGCGTGTGGATTCT 1330
QY 1105 CCCATGCTGAGCCGTCACGGGAACGCGGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1164
Db |||||
QY 1331 CCCATGCTGAGCCGTCACGGGAACGCGGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1390
QY 1165 ATCACCAGTCCGGGGTGGTCCCTCTACCCACCGAGCGGCTTGGAGATGGCC 1224
Db |||||
QY 1391 ATCACCAGTCCGGGGTGGTCCCTCTACCCACCGAGCGGCTTGGAGATGGCC 1450
QY 1225 CAGCACACCCAGAGATCCCGTAGCGTCACTGAGAGCTTCCAGGGTCTGTCTCTCAGGCCCT 1284
Db |||||
QY 1451 CAGCACACCCAGAGATCCCGTAGCGTCACTGAGAGCTTCCAGGGTCTGTCTCTCAGGCCCT 1510
QY 1285 CTAAGCAGCCCAAGAGTCCGCTCTTTTCTTTTCCCGGAGCCGGGGCTGGAGATGAG 1344
Db |||||
QY 1511 CTAAGCAGCCCAAGAGTCCGCTCTTTTCTTTTCCCGGAGCCGGGGCTGGAGATGAG 1570
QY 1345 GCTCCAGGCGGGGCTCCCGACTTCCAAAGCGAGAGCTGCCTTCTTCGGGGGCCCCAGG 1404
Db |||||
QY 1571 GCTCCAGGCGGGGCTCCCGACTTCCAAAGCGAGAGCTGCCTTCTTCGGGGGCCCCAGG 1630
QY 1405 GGTGGGGGCGCGGGGAGAGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCCGGC 1464
Db |||||
QY 1631 GGTGGGGGCGCGGGGAGAGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCCGGC 1690
QY 1465 CCCCCAGAGTCCCGGGCTCTCTGCGGGGACCCCTTGTGCACTCGCTCTGACACGCGCC 1524
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QY 1525 CGGGCAGTCCACCGGACCCCGGGGACAAACACACCCCGAGCCCGGGGGTGGCGTC 1584
Db 1751 CGGGCAGTCCACCGGACCCCGGGGACAAACACACCCCGAGCCCGGGGGTGGCGTC 1810
QY 1585 GGGGAGCGCGCTGAGGAGTGTCTCAACTCCATCCGCAACAGCTTCTGCGGCTCCCT 1644
Db 1811 GGGGAGCGCGCTGAGGAGTGTCTCAACTCCATCCGCAACAGCTTCTGCGGCTCCCT 1870
QY 1645 CGCTTTCACCGGCGCAAGATGCAAGTCCGCTGAGGAGATGTCAGCTTGAAGCCA 1704
Db 1871 CGCTTTCACCGGCGCAAGATGCAAGTCCGCTGAGGAGATGTCAGCTTGAAGCCA 1930
QY 1705 GAGTCTCTCCCGGAGCTGGCAAAACGCTCTGCTTGGGAACTTCACTCTCTTGGACAAA 1764
Db 1931 GAGTCTCTCCCGGAGCTGGCAAAACGCTCTGCTTGGGAACTTCACTCTCTTGGACAAA 1990
QY 1765 GAAGAACAAATATCTCTGTGTAAAGGACAAACCTCTCAGCAGCATCAAGACAGCATC 1824
Db 1991 GAAGAACAAATATCTCTGTGTAAAGGACAAACCTCTCAGCAGCATCAAGACAGCATC 2050
QY 1825 GTCCATGCTTCTGTGATCCCGAGCTGAGTCAAGTGTCTGTCAAGACACAGCTTC 1884
Db 2051 GTCCATGCTTCTGTGATCCCGAGCTGAGTCAAGTGTCTGTCAAGACACAGCTTC 2110
QY 1885 AGGGCCGAGTACAAAGGACAGTGGCGGCCCTCTCTTCCAAAGCCGCTCGCTTCCAG 1944
Db 2111 AGGGCCGAGTACAAAGGACAGTGGCGGCCCTCTCTTCCAAAGCCGCTCGCTTCCAG 2170
QY 1945 GTGGACATCAGCTCTCTGAGGTCAGAGCCCTCCCGGAGCGGACGGCAGCGAGGT 2004
Db 2171 GTGGACATCAGCTCTCTGAGGTCAGAGCCCTCCCGGAGCGGACGGCAGCGAGGT 2230
QY 2005 GGTGGACATCTACTCGGTCACTTCACTCTCATCTCGGGTCCAGCCGCTCGGTTCAGCGA 2064
Db 2231 GGTGGACATCTACTCGGTCACTTCACTCTCATCTCGGGTCCAGCCGCTCGGTTCAGCGA 2290
QY 2065 GTGGTGGAGACCATCCAGGACAGTCTCTGAGCATCTCATGACAGCCCTCCGTGAGCGCC 2124
Db 2291 GTGGTGGAGACCATCCAGGACAGTCTCTGAGCATCTCATGACAGCCCTCCGTGAGCGCC 2350
QY 2125 CTGGCAGACGAGAAACGGGGCCAGACCCGGCTGCTGGTCCGCCACCCCGAAGCCTG 2184
Db 2351 CTGGCAGACGAGAAACGGGGCCAGACCCGGCTGCTGGTCCGCCACCCCGAAGCCTG 2410
QY 2185 CAGCCCCACCCCGCGCCCGAGACCCAGAGCTGAGAGCTCTCCCGCCGAGGCCCCCCC 2244
Db 2411 CAGCCCCACCCCGCGCCCGAGACCCAGAGCTGAGAGCTCTCCCGCCGAGGCCCCCCC 2470
QY 2245 AAGGACAAAGAGTCTCTGGCCACCAAGGGACCCCTCTGCGCTGA 2289
Db 2471 AAGGACAAAGAGTCTCTGGCCACCAAGGGACCCCTCTGCGCTGA 2515
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RESULT 14

ADQ89183
ID ADQ89183 standard; cDNA; 2980 BP.

XX ADQ89183;

AC ADQ89183;

XX 21-OCT-2004 (first entry)

XX Human urological disorder related protein 55053 encoding cDNA SEQ.135.

XX urological disorder; uropathic; cytostatic; urinary incontinence;

XX benign prostatic hyperplasia; human; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FH 86. .2422

XX CDS

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FT      /*tag= a
PN      /product= "urological disorder related protein 55053"
XX      WO2004065576-A2.
XX      05-AUG-2004.
XX      14-JAN-2004; 2004WO-US000750.
XX      15-JAN-2003; 2003US-0440318P.
XX      04-FEB-2003; 2003US-0444783P.
XX      27-MAR-2003; 2003US-0457901P.
XX      08-MAY-2003; 2003US-0468775P.
XX      19-MAY-2003; 2003US-0471614P.
XX      16-JUN-2003; 2003US-0478422P.
XX      18-JUL-2003; 2003US-0488529P.
XX      30-JUL-2003; 2003US-0491156P.
XX      02-SEP-2003; 2003US-0499594P.
XX      26-SEP-2003; 2003US-0506332P.
XX      (MILL-) MILLENNIUM PHARM INC.
XX      Karicheti V, Silos-Santiago I, Eliasof SD;
XX      WPI: 2004-562167/54.
XX      P-PSDB; ADQ89184.
XX      Use of polypeptides related to urological disorders, e.g. 44390, 54181,
PT      211 or for identifying a compound capable of treating a urological
PT      disorder or identifying and treating a subject having a urological
PT      disorder.
XX      Claim 1; SEQ ID NO 135; 542pp; English.
XX      The present invention describes the use of polypeptides related to
CC      urological disorders for identifying a compound capable of treating a
CC      urological disorder, identifying a subject having a urological disorder,
CC      or treating a subject having a urological disorder. Also described: (1) a
CC      method for identifying a compound capable of treating a urological
CC      disorder; and (2) a method for identifying a subject having a urological
CC      disorder. The compound has uteropathic and cytostatic activities. The
CC      polypeptides related to urological disorders are useful for identifying a
CC      compound capable of treating a urological disorder, identifying a subject
CC      having a urological disorder, or treating a subject having a urological
CC      disorder. Disorders include urinary incontinence and benign prostatic
CC      hyperplasia. The present sequence encodes a human urological disorder
CC      related protein, which is used in the exemplification of the present
CC      invention.
XX      Sequence 2980 BP; 625 A; 959 C; 886 G; 510 T; 0 U; 0 Other;
XX      Query Match      88.3%; Score 2020.2; DB 13; Length 2980;
XX      Best Local Similarity 99.9%; Pred. No. 0;
XX      Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX      265 TTTAGGTACCTGGTTCTGGAGACAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 324
XX      398 TATTGTGTTACCTGGTTCTGGAGACAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 457
XX      325 AAGGGAGAGCTAGCGCCCAAGAGAGCGCCGAAAGTTCTTCGCGAGATTGTCTGCGCTG 384
XX      458 AAGGGAGAGCTAGCGCCCAAGAGAGCGCCGAAAGTTCTTCGCGCAGATTGTCTGCGCTG 517
XX      385 GACTTCTGCCACAGCTACTCCATCTGCGACAGACCTTAAGCCCGAGAACCTGCTTTTG 444
XX      518 GACTTCTGCCACAGCTACTCCATCTGCGACAGACCTTAAGCCCGAGAACCTGCTTTTG 577
XX      445 GATGAGAAAAACAACATCCGATTCGAGACTTCGGGCATGGCGTCCCTCGAGAGTGGGGGAC 504
XX      578 GATGAGAAAAACAACATCCGATTCGAGACTTCGGGCATGGCGTCCCTCGAGAGTGGGGGAC 637
XX      505 AGCCTCTGGAGACCAAGCTGCGGGTCCCCCAATTATTCGCTGTCCAGAGGTGATTAAAGGGG 564
Db      638 AGCCTCTGGAGACCAAGCTGCGGGTCCCCCAATTATTCGCTGTCCAGAGGTGATTAAAGGGG 697
Qy      565 GAAAAATATGATGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTCTTCGCGCTG 624
Db      698 GAAAAATATGATGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTCTTCGCGCTG 757
Qy      625 CTGCTGGGGGCTCTGCGCTTTTGATGACGACAACTCCGCGAGCTGTGGAGAGAGTGAAG 684
Db      758 CTCGTGGGGGCTCTGCGCTTTTGATGACGACAACTCCGCGAGCTGTGGAGAGAGTGAAG 817
Qy      685 CGGGGCGCTCTTCACATGCGCCCACTTCATTCTCCAGATTGCCAGAGCTCTCTCAGGGGA 744
Db      818 CGGGGCGCTCTTCACATGCGCCCACTTCATTCTCCAGATTGCCAGAGCTCTCTCAGGGGA 877
Qy      745 ATGATCGAAGTGGAGCGCCGAAAAAGGCTCAGTCTGTGGAGCAAAATTCAGAAACATCTTTGG 804
Db      878 ATGATCGAAGTGGAGCGCCGAAAAAGGCTCAGTCTGTGGAGCAAAATTCAGAAACATCTTTGG 937
Qy      805 TACCTAGCGGGGAAAACAGAGCGAGACCCGCTGCTGTGGAGCAGCCCTCTGCGCGCGGGTA 864
Db      938 TACCTAGCGGGGAAAACAGAGCGAGACCCGCTGCTGTGGAGCAGCCCTCTGCGCGCGGGTA 997
Qy      865 GCCATGCGGAGCGCTGCCATCCAAACGAGAGCTGACCCCGACCGTCTTAGAGAGCATGSCA 924
Db      998 GCCATGCGGAGCGCTGCCATCCAAACGAGAGCTGACCCCGACCGTCTTAGAGAGCATGSCA 1057
Qy      925 TCACTGGGCTGCTTTCAGGGACCGGAGAGCTGTCATCGCGAGCTGCGCAGTGGAGAGGAG 984
Db      1058 TCACTGGGCTGCTTTCAGGGACCGGAGAGCTGTCATCGCGAGCTGCGCAGTGGAGAGGAG 1117
Qy      985 AACCAAGAAAAGATGATATATATCTGCTTTTGGATCGAAGAGCGGTATCCAGCTGT 1044
Db      1118 AACCAAGAAAAGATGATATATATCTGCTTTTGGATCGAAGAGCGGTATCCAGCTGT 1177
Qy      1045 GAGGACGAGACCTGCTCCCGGAAATGATGTTGACCCCGGAGAGCGGTGCGATTCT 1104
Db      1178 GAGGACGAGACCTGCTCCCGGAAATGATGTTGACCCCGGAGAGCGGTGCGATTCT 1237
Qy      1105 CCATGCTGAGCGCTCAACGGGAAAGCGGACGAGCGGAAAGTCCATGGAAGTCTCTGAGC 1164
Db      1238 CCATGCTGAGCGCTCAACGGGAAAGCGGACGAGCGGAAAGTCCATGGAAGTCTCTGAGC 1297
Qy      1165 ATCAACGATCGCGGGGTGTGCTCCCTGTATACCAACGAGCGGCTTTGGAGATGCGC 1284
Db      1298 ATCAACGATCGCGGGGTGTGCTCCCTGTATACCAACGAGCGGCTTTGGAGATGCGC 1357
Qy      1225 CAGCAGACGAGATCCCGTAGGTCAGTGGAGCTTCCAGGGTCTGTCTCCAGGCT 1284
Db      1358 CAGCAGACGAGATCCCGTAGGTCAGTGGAGCTTCCAGGGTCTGTCTCCAGGCT 1417
Qy      1285 CTAAAGAGCCCAAGAGTCCGCTCTTTTCTTTTTCACCGAGCGGGGCTGGAGATGAG 1344
Db      1418 CTAAAGAGCCCAAGAGTCCGCTCTTTTCTTTTTCACCGAGCGGGGCTGGAGATGAG 1477
Qy      1345 GCTCGAGGCGGGGCTCTCCCGACTTCCAAACGAGACGCTGCTTCTCGGGGCCCCCAGG 1404
Db      1478 GCTCGAGGCGGGGCTCTCCCGACTTCCAAACGAGACGCTGCTTCTCGGGGCCCCCAGG 1537
Qy      1405 GGTGGGGGCGCGGGGAGAGCGCCCGCGCCCGCGCTCCAGCTCCACACCGCTGCGCGGC 1464
Db      1538 GGTGGGGGCGCGGGGAGAGCGCCCGCGCCCGCGCTCCAGCTCCACACCGCTGCGCGGC 1597
Qy      1465 CCCCAGGCTCTCCCGGCTCTCTTGGCGGAGCCCTTTCGCTCTGCTGACACAGCGCC 1524
Db      1598 CCCCAGGCTCTCCCGGCTCTCTTGGCGGAGCCCTTTCGCTCTGCTGACACAGCGCC 1657
Qy      1525 CGGGCCAGTCCACCGGAGACCCCGGGGAAACACACACCCCGGCGGGTGGGGTGC 1584
Db      1658 CGGGCCAGTCCACCGGAGACCCCGGGGAAACACACACCCCGGCGGGTGGGGTGC 1717
Qy      1585 GGGGAGCGCGCTGGAGAGTCTGCTCAACTCAGTCGGAACAGCTTCTCGGGTCCCTCCCT 1644
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[illegible]

QY 625 CTCGTGGGGCTCTGCCCTTTGATGACGACAACTCCGCCAGCTCTGGAGAAAGTGA 684
Db |||||
QY 758 CTCGTGGGGCTCTGCCCTTTGATGACGACAACTCCGCCAGCTCTGGAGAAAGTGA 817
Db |||||
QY 685 CGGGCGCTTTCCACATGCCCCCACTTCAATCTCCAGATTGCCAGAGCTCTCTGAGGGA 744
Db |||||
QY 818 CGGGCGCTTTCCACATGCCCCCACTTCAATCTCCAGATTGCCAGAGCTCTCTGAGGGA 877
Db |||||
QY 745 ATGATCGAAGTGGAGCCGGAAGAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG 804
Db |||||
QY 878 ATGATCGAAGTGGAGCCGGAAGAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG 937
Db |||||
QY 805 TACCTAGCGGGAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTTGGCCGCGGGTA 864
Db |||||
QY 938 TACCTAGCGGGAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTTGGCCGCGGGTA 997
Db |||||
QY 865 GGCATGGGAGCTGCCATCCAAACGAGAGCTGACCCCGACGCTCTTAGAGAGCATGGCA 924
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Db |||||
QY 925 TCATCGGCTGCTTCAGGACCCGAGAGGCTGCATCGCGAGCTGCGCAGTGGAGGAG 984
Db |||||
QY 1058 TCATCGGCTGCTTCAGGACCCGAGAGGCTGCATCGCGAGCTGCGCAGTGGAGGAG 1117
Db |||||
QY 985 AACCAAGAAAGATGATATATATCTGCTTTGGATCGGAAGAGCGGTATCCAGGTGT 1044
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Db |||||
QY 1045 GAGCAGCAGGACCTGCCCTCCCGGAATGATGTTCAGCCCGCCCGAAGCGGTGCGATTCT 1104
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Db |||||
QY 1105 CCATGTGTAGCCGCTCAGGGAAGCGGCGACAGAGCGGGAAGTCCATGGAAGTCTTGAGC 1164
Db |||||
QY 1238 CCATGTGTAGCCGCTCAGGGAAGCGGCGACAGAGCGGGAAGTCCATGGAAGTCTTGAGC 1297
Db |||||
QY 1165 ATCACGATGCGGGGCTGCTGCTCTCTGATACCCACCGAGCGGCTTGGAGATGCGC 1294
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Db |||||
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Db |||||
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Db |||||
QY 1418 CTAAAGCAGCCCAAGGAGTCCGCTCTTTTCTTTTTCACCGAGCGGGGCTGGAGATGAG 1477
Db |||||
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Db |||||
QY 1478 GCTCAGGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTCTGCGGGCCCCAGG 1537
Db |||||
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Db |||||
QY 1465 CCCCAGGCTCCCGCGCTCTCTGCGGGGACCCCTTGACCTCGCTCTGCACACGCCC 1524
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Db |||||
QY 1525 CGGGCCAGTCCACCGGAGCCCGGGGACAAACACACCCCGAGCCCGGGGCTGGGCTC 1584
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QY 1658 CGGGCCAGTCCACCGGAGCCCGGGGACAAACACACCCCGAGCCCGGGGCTGGGCTC 1717
Db |||||
QY 1585 GGGGAGCGGCTGGAGAGTGTCTCAATCCATCGGCAACAGCTTCTGGGCTCCCT 1644
Db |||||
QY 1718 GGGGAGCGGCTGGAGAGTGTCTCAATCCATCGGCAACAGCTTCTGGGCTCCCT 1777
Db |||||
QY 1645 CGCTTTTCAACCGGCAAGATCAGGTCCCTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1704
Db |||||
QY 1778 CGCTTTTCAACCGGCAAGATCAGGTCCCTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1837
Db |||||

QY 1705 GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTTCGGGAACCTTCATCTCTCTGACAAA 1764
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QY 1838 GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTTCGGGAACCTTCATCTCTCTGACAAA 1897
Db |||||
QY 1765 GAAGAACAAATATTTCTCTGCTAAAGGACAAAACCTCTCAGCAGCATCAAAAGCAGACATC 1824
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QY 1898 GAAGAACAAATATTTCTCTGCTAAAGGACAAAACCTCTCAGCAGCATCAAAAGCAGACATC 1957
Db |||||
QY 1825 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCAAGTGTGTGTCAAGCAGCAGCTTC 1884
Db |||||
QY 1958 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCAAGTGTGTGTCAAGCAGCAGCTTC 2017
Db |||||
QY 1885 AGGSCCAGTACAGGCGCAGTGGGGCCCTCTCCCTCTTCAAAGCCCGCTCCGCTTCCAG 1944
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QY 2018 AGGSCCAGTACAGGCGCAGTGGGGCCCTCTCCCTCTTCAAAGCCCGCTCCGCTTCCAG 2077
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QY 1945 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGT 2004
Db |||||
QY 2078 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGT 2137
Db |||||
QY 2005 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGTTCAAGCGA 2064
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QY 2138 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGTTCAAGCGA 2197
Db |||||
QY 2065 GTGGTGGAGACCATCCAGGCGACAGCTCTGAGCACTCATGACAGCCCTCCGTCGAGGCC 2124
Db |||||
QY 2198 GTGGTGGAGACCATCCAGGCGACAGCTCTGAGCACTCATGACAGCCCTCCGTCGAGGCC 2257
Db |||||
QY 2125 CTGGCAGACGAGAAACGGGGCCAGACCCGGGCTGCTGGTGGCCCAACCCCGAAGCCTG 2184
Db |||||
QY 2258 CTGGCAGACGAGAAACGGGGCCAGACCCGGGCTGCTGGTGGCCCAACCCCGAAGCCTG 2317
Db |||||
QY 2185 CAGCCCCCAGCCCGCCCGCCAGACCCAGAGTGAAGCTCTCTCCCGCGAGGCCCCCC 2244
Db |||||
QY 2318 CAGCCCCCAGCCCGCCCGCCAGACCCAGAGTGAAGCTCTCTCCCGCGAGGCCCCCC 2377
Db |||||
QY 2245 AAGGACAAAGAGTCTCTGGGCCAACCAACGGGAGCCCTCTGCGCCTGA 2289
Db |||||
QY 2378 AAGGACAAAGAGTCTCTGGGCCAACCAACGGGAGCCCTCTGCGCCTGA 2422
Db |||||

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